

Best Local Similarity

Matches	941: Conservative	0: Mismatches	0: Indels	0: Gaps
Db	1	MASPRSSQGPPEPPPPPPARLLLLLLLLPLPLPLAGAMGAMGAPRPPSSPLSTMG	60	
Qy	1	MASPRSSQGPPEPPPPPPARLLLLLLLLPLPLPLAGAMGAMGAPRPPSSPLSTMG	60	
Db	61	IMPLTRKVAKSGTGGVLPAVELAEQIRNSSLRPYFLDLRLDYDECDNAKGKATYDA	120	
Qy	61	IMPLTRKVAKSGTGGVLPAVELAEQIRNSSLRPYFLDLRLDYDECDNAKGKATYDA	120	
Db	121	IKYGNHLMVFGVCPSTYSITIAESLQGMNLYVLSFAATPYVLADKKKYPFEFTYVSDN	180	
Qy	121	IKYGNHLMVFGVCPSTYSITIAESLQGMNLYVLSFAATPYVLADKKKYPFEFTYVSDN	180	
Db	181	AVNPAIILKLKKYQMKRGTLLDQVQRSEVRNDLTGLYGEDIEISDTESFSDPCTSV	240	
Qy	181	AVNPAIILKLKKYQMKRGTLLDQVQRSEVRNDLTGLYGEDIEISDTESFSDPCTSV	240	
Db	241	KLKLGNDVRIILGFDONMAAKVFCACAEENMYGSKYQWIIIPGYEPSWMEQVHTEANS	300	
Qy	241	KLKLGNDVRIILGFDONMAAKVFCACAEENMYGSKYQWIIIPGYEPSWMEQVHTEANS	300	
Db	301	RLRLRNLLAAMGTVGVNPEPLSSKOITIGSKPPOQERETNNKRSVGSKFHGAAYD	360	
Qy	301	RLRLRNLLAAMGTVGVNPEPLSSKOITIGSKPPOQERETNNKRSVGSKFHGAAYD	360	
Db	361	GIWIVAKTLQRAMETLHAASSRHQRKODPNYDHTLGRILNAMETNFGYTGCVFRNG	420	
Qy	361	GIWIVAKTLQRAMETLHAASSRHQRKODPNYDHTLGRILNAMETNFGYTGCVFRNG	420	
Db	421	ERMGTIKFTQFODSRKVKGEYNAVADLTLEIINDTIRFQSEBPPDKTIIIEQLRKISLP	480	
Qy	421	ERMGTIKFTQFODSRKVKGEYNAVADLTLEIINDTIRFQSEBPPDKTIIIEQLRKISLP	480	
Db	481	LVSIISALTILGMIWASAFLEPNIKRNROKLIKMSPPMNNLIIIGWLSVASFLEGLD	540	
Qy	481	LVSIISALTILGMIWASAFLEPNIKRNROKLIKMSPPMNNLIIIGWLSVASFLEGLD	540	
Db	541	GSFVSEKTEFEELCTVRTWIIIVGYTTAFGAMFAKRWHAIFKNVKKMKKIIIKDQKLLVI	600	
Qy	541	GSFVSEKTEFEELCTVRTWIIIVGYTTAFGAMFAKRWHAIFKNVKKMKKIIIKDQKLLVI	600	
Db	601	VGGMLLIDICILICQWADPLRRTVEKYSMEBPDAGRDISIRPLEHCENHTMTWLGIV	660	
Qy	601	VGGMLLIDICILICQWADPLRRTVEKYSMEBPDAGRDISIRPLEHCENHTMTWLGIV	660	
Db	661	VAYKGLIMEFGFGLAMERNVSIPLALNSKYIGMSVYVWVGIMCIIIGAIVSFLTRQPPVQ	720	
Qy	661	VAYKGLIMEFGFGLAMERNVSIPLALNSKYIGMSVYVWVGIMCIIIGAIVSFLTRQPPVQ	720	
Db	721	FCIVALVIFCSTITCLVFEVFKLTLELRNPDAQNRFOFTONOKKEDSTSTSVSY	780	
Qy	721	FCIVALVIFCSTITCLVFEVFKLTLELRNPDAQNRFOFTONOKKEDSTSTSVSY	780	
Db	781	NOASTSRLEGLQSENNHRLRMKITELDKDLLEVYMLQDTPERTYVIKONHYQELNDIILNL	840	
Qy	781	NOASTSRLEGLQSENNHRLRMKITELDKDLLEVYMLQDTPERTYVIKONHYQELNDIILNL	840	
Db	841	GNFTSTDDGKAILKNHLDQNPOLQWNTTPEBTRTKDPEIDINSPEHQRRLSIDPLIH	900	
Qy	841	GNFTSTDDGKAILKNHLDQNPOLQWNTTPEBTRTKDPEIDINSPEHQRRLSIDPLIH	900	
Db	901	HAYLPSIGGVADSCVSPCVSPASPAPRHHRRHVPSPFVWVSGL	941	
Qy	901	HAYLPSIGGVADSCVSPCVSPASPAPRHHRRHVPSPFVWVSGL	941	
RESULT	2	PRELIMINARY:	PRT:	940 AA.
AC	088871:			
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)			

DE	GABA-B RECEPTOR GB2.
OC	Rattus norvegicus (Rat).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE= CEREBRAL CORTEX:
RA	CLARK J.C., LAM A., BONNER T.I.;
RT	"g92, a second GABA-B receptor."
RL	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AF058795; AAC63994.1; -
DR	PFAM: PF00003; 7tm_3; 1.
DR	PFAM: PF01094; ANF_receptor; 1.
SQ	SEQUENCE 940 AA; 105762 MW; 94C83CC1 CRC32;
Query Match	97.9%; Score 6760; DB 11; Length 940;
Best Local Similarity	97.6%; Pred. NO. 0.00e+00;
Matches 918; Conservative	16; Mismatches 6; Indels 1; Gaps 1;
Dd	1 MASPPSSGQP-RPPPPPARRLLPLLSILLMLWAGAMGWTRGADPPSPSSPLSIMG 59
Oy	1 MASPPSSGQGP PPPPPPPRRLLLLLLLPLLP LLPLA PGMWGARGARPPSPSSPLSIMG 60
Dd	60 LMPLEKFAKSGSIGGVLPAYELAEQRNSILRPYFLDIRLYDTGCNNAKGIGKATYDA 119
Oy	61 LMPLEKFAKSGSIGGVLPAYELAEQRNSILRPFLDIRLYDTGCNNAKGIGKATYDA 120
Dd	120 IKYGNNHLMVFGVCPSTYSIIAESLGQMNLVOLSFATTPPVYLADKKKPYFFPTVESDN 179
Oy	121 IKYGNNHLMVGGVCPSTYSIIAESLGQMNLVOLSFATTPPVYLADKKKPYFFPTVESDN 180
Dd	180 AVNPAILKLKHFRNRVGTLLTDXXRFSEVRNDLTGYLVGEDIEISDTSFSNDPCTSV 239
Oy	181 AVNPAILKLKHGYKRVGTLLTDXXRFSEVRNDLTGYLVGEDIEISDTSFSNDPCTSV 240
Dd	240 KTLKNDVRITLIGDPDQNMNAKVPCCAFEESMGSKYOMIIPGYEPAEMQOVAVEANSS 299
Oy	241 KTLKNDVRITLIGDPDQNMNAKVPCCAVEENMNGSKYOMIIPGYEPMQOVAVEANSS 300
Dd	300 RLRLRSLLAAMEGYIGVDFEPLTSSKOITLISGKTPOQFEREYNKRSGVGFSKHHGYAD 359
Oy	301 RLRLRNLLAAMGYIGVDFEPLTSSKOITLISGKTPOQERYENKNRSGVGFSKHHGYAD 360
Dd	360 GIWVIATAKTLORAMETLHAASSRHRIQDFNYTDHTLGKIILNAMNETNFPGVTGGVFRNG 419
Oy	361 GIWVIATAKTLORAMETLHASRRHORIDFNNTDHTLGRIILNAMNETNEFGVTGGVFRNG 420
Dd	420 EWMGITIKTFOPDSSSEVVYGEYNAADPLEIINPIIRQGSEPPDKTIILEQLRKISLP 479
Oy	421 EWMGITIKTFOPDSSSEVVYGEYNAADPLEIINDPIIRQSGSEPPDKTIILEQLRKISLP 480
Dd	480 LYSIISALTIIGMIASAFLEFNINRNROKLIKMSPPMNMLIILGMLSYASIFLEGLD 539
Oy	481 LYSIISALTILGMIASAFLEFNINRNROKLIKMSPPMNMLIILGMLSYASIFLEGLD 540
Dd	540 GSFESEKTEPETLCYRTWLIVGYTTAAGAMFAKTWRVHALFKNVKMKKLIIDOKLLVI 599
Oy	541 GSFESEKTEPETLCYRTWLIVGYTTAAGAMFAKTWRVHALFKNVKMKKLIIDOKLLVI 600
Dd	600 VEGMLIIDICILICQAOADPLRLRYERYSMEDPAGRIDISIRPLLHCENTHMTIWGIY 659
Oy	601 VEGMLIIDICILICQAOADPLRLRYEKEYSMEDPAGRIDISRPLLEHCENTHMTIWGIY 660
Dd	660 VAYKGGLMFEGGLEMERNNVISPALNDSKYIGMSVYWIMCIIGAASFLLTDQPRVQ 719
Oy	661 VAYKGGLMFEGGLEMERNNVISPALNDSKYIGMSVYWIMCIIGAASFLLTDQPRVQ 720
Dd	720 PCIVAVLIIIFGCTITLCVPEVKILTLETNPDAATONRRFOFOTONOKKEDSTSTVSIV 779
Oy	721 PCIVAVLIIIFGCTITLCVPEVKILTLETNPDAATONRRFOFOTONOKKEDSTSTVSIV 780
Dd	780 NOASTSRLEGLOS ENHRRLRMKITTELKDULEEVYTMOLQDTPERTTY I KONHY QEIINDIIST 839

QY 781 NOASTSRLEGLSEHNRLRMKITELDKDELEVWQLODPTREKTYIKONHYGELNDILNL 840
Db 840 GNFTESTDGGKAILKNHLDONPOLDMNTTEPRTCKDPEDINSEPHORLSLOPLIH 899
QY 841 GNFTESTDGGKAILKNHLDONPOLDMNTTEPRTCKDPEDINSEPHORLSLOPLIH 900
Db 900 HAYLPISIGVDASVPCVSPASPRHRHVRPSPFRVMSGL 940
QY 901 HAYLPISIGVDASVPCVSPASPRHRHVRPSPFRVMSGL 941
RESULT 3
ID 09Y133 PRELIMINARY; PRT; 1221 AA.
AC 09Y133:
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE BCDA.GH07312.
GN BCDA.GH07312.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RA RUBIN G.M., WAN K.H., HARVEY D., LEWIS S.E., BROKSTEIN P., TSANG G.,
AGRAYANI A., ARCAINA T.T., BAXTER E., BLAZER R.G., BOTENHOFF C.,
CHAPPE M., CHAVEZ C., CHEW M., DOYLE C.M., FARAN D.E., FRISSE E.,
RA GALLE R., GEORGE R.A., HARRIS N.L., HOSKINS R.A., EVANS-HOLM M.,
RA HOUTON K.A., HUMMASTI S.R., KIM E., LI P., MOSHREFI M., PACIER J.M.,
RA PARK S., SEQUIDIRA A., SETHI H., SNIR E., SVIRSKAS R.R., WEINBURG T.,
RA CELINKER S.E.;
RT "Full length Drosophila melanogaster cDNA sequence."
RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF145639; AAD38614.1; -
SQ SEQUENCE 1221 AA; 138124 MW; CE3B7865 CRC32;
Query Match 32.7%; Score 2255; DB 5; Length 1221;
Best Local Similarity 41.8%; Pred. No. 0.00e+00;
Matches 325; Conservative 196; Mismatches 236; Indels 21; Gaps 17;
Db 18 M5TAGCGRTAKRSD-VYIAGFFPYGDCVENSYTGRCMPSPKALGHVNHGKILANYRLH 76
QY 42 WARGAPRRPPSSPLSLIMKIMPLTEKVAKGSTGRVLAPELAIQIRNES-LLRPFELD 100
Db 77 MWMNDTQCAAVGKVSFEDMHSKPNKVMFLGSACTHTDPIAKASKMHMLTQLSYADTH 136
QY 101 LRLYDECDNAKGLKAFYDAIKYGRPHMLVFGVCPSVTSIAESLQGMNLVQLSFAATT 160
Db 137 PMFT-KDAEPNFRVYVPSNAPNARLALKFENMTRVGYQNEPRISLPHNHVADLD 195
QY 161 PVLAKKKKPYFFRRVPSNANVPAIILKLKHVOMKRVGTLODVRSEVNDLGVLY 220
Db 196 AMEVEVETQSVNDVAESLKKLREKDVRIIGNFNEHARKAFCEAVKLDYGRAYOML 255
QY 221 GEDIEISDIESTESNDPCTSVKLLKGNDRYIILGDPDQNAKAVFCCAEENNYGSKYOMI 280
Db 256 IMATYSTDMW-V-TQ-DSE-CSEVEIATALEGAILVDLPLSTSGDITVAGITADEVLY 311
QY 281 IGWEPSPWMEQVHTEANSRCLRNLLAAMEGYIGVDEPELSSNOIKTISKTPQOYER 340
Db 312 EYDRLR-GTEYSRPHGYTYDGIWA-A-AL--AIQYV-AEKREDLLTHEDYRVKDMESVFL 365
QY 341 ELNNKKSQGVGPKFPGYADGIMVIAKTLQRAMETLHASSRHQRLODFWYTHHTGRILL 400
Db 366 EALRNTSEFGVGPVRFVYNNERKANLIMQFOLGOMEKIGEYHSQKSHDLSIGKPVKV 425
QY 401 NMANENFEGVIGVYFNGERNGIKTKTFQODSRKVGKGTNAVAADLLET-INDTIRQ 459
Db 426 GTPPKDRTLLYIEHSQVNPITYIVSASAVIGVIAATVLAFTKYNRQRYIKMSSPRL 485
QY 460 GSEPPDKTKILLQLRKISLPLYSILSALTILGIMASAFLEPFNKIKNRQKIKKSSPYM 519

Db 486 NNLIIYGOMMYLSTIFIGLDTLSSVAAPPYICTARAWILMGFSFGAMFSKTRVH 545
QY 520 NNLIIYGOMMYLSTIFIGLDTLSSVAAPPYICTARAWILMGFSFGAMFSKTRVH 579
Db 546 SIPTDLKINKKVIKIDYOLFVWVGLAIDAIIITTOIADPFYRETKOLPLHENDID-P 604
QY 580 AIFNFKKKKKIINDQKLVIYVGMILLDLCILCQWAVDPL-RRYEXKSMEDPACGRD 638
Db 605 VLVIPENYCOSEHMTTFVSTIYAYKGLLVGAFAMETRHHSIPALNDSKHIGSVYN 664
QY 639 ISIRPLEHCENFMTITWGLIVAYKGLMLFGCFLMETRHNVSIPALNDSKHIGSVYN 698
Db 665 VEITCIGAATSLVSRKDLVFLISFETICTATLCVFPVKLVELKRNPGVY-DK 723
QY 699 VGICITIGAAVSFLTRDPNPVOCIVAVIIFCSTITLCLVFPVKLITLKRNPDAQNR 758
Db 724 RVKATLRPMKNGRRDSSVCELEQ----RLNDVKNTRCKRRKALMEKENELQALIRKL 777
QY 759 RFOFTQNGKREDSKTSSTSVNQASTSRLEGLSEHNRLRMKITELDKDELEVWQLO 816
RESULT 4
ID 09Z308 PRELIMINARY; PRT; 812 AA.
AC 09Z308:
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
DE GABAB RECEPTOR ID.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-CEREBELLUM;
RC MEDLINE; 99092370.
RA ISOMOTO S., KAIKARA M., SAKURAI-YAMASHITA Y., NAGAYAMA Y., UZONO Y.,
RA YANO K., TANIYAMA K.;
RT "Cloning and tissue distribution of novel splice variants of the rat
GABAB receptor."
RL Biochem. Biophys. Res. Commun. 253:10-15(1998).
DR EMBL; AB016161; BAA34709.1; -
KW Receptor.
SQ SEQUENCE 812 AA; 90920 MW; 566BF90A CRC32;
Query Match 24.5%; Score 1690; DB 11; Length 812;
Best Local Similarity 35.4%; Pred. No. 0.00e+00;
Matches 268; Conservative 194; Mismatches 271; Indels 23; Gaps 21;
Db 2 GGPGCTPVGMPRLDULLVMAGVAPVMASSHPLPRPHRPVPRPSSERAVYIGAL-FP 60
QY 11 GPPPPPPPPARLLLLLLPL-LPL-APGAWGNARQAPR-PP-PSSPPULSI-MGLMPLT 65
Db 61 MSGGMPG-GQACOPAVEMALEDVNSRDLIDPYELKLHDSKCDPQCATRYLEYELYN 119
QY 66 KEVAKGSGRGVLAPELAIQIRNE-SLRRPYLDLRIDYEDCNKAGKAFDAIKYG 124
Db 120 PIKTIIMP-G-SSVSTVIAEARMNMLIVSYGSSPALSNRQFPFFFTPTSPATLANP 178
QY 125 PNHLLVFGVCPVSTSIASLSQGMNLVQLSFAATTPLADKKKPYFFRRVPSDNAVNP 184
Db 179 TRVLFEXMKKKKATATIOOTTEVFTSHLDLEEVYKRGAGITITROSFPSPRAVPYKLP 238
QY 185 AILKLKHVOMKRVGTLODVRSEVRANDLTGVLEGDEIESTSEFSNDPCTSVKLLK 244
Db 239 RODARIIVGLFYETEARVCEVYKERLFGKKYWMFLIGWYADWMP-KTY-DP-SINCTV 295
QY 245 GNDRIIILGQDQNAKAVFCCAEENNYGSKYMIIPGWTEPSWMOYHTEANSRCLR 304
Db 296 EEMTEAVGSHITTEIVMLNPANTRISNMTSQEFVEKRLKLRKHHPRETGQFQAPLAYD 355
QY 305 KNLLAAMEGYIGVDEPELSSKOIKTISKTPQOY-EREYNN-KRSGVGPSEKFH-G-YAID 360
Db 356 AIAKALALANKTSG--GGRSGVRLDEPNYNNQITTDQIYAAHSSSFEGVSGHYVNDAS 413

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OY 361 GIWIAKTLQRAMETLHASRHRQRIODFNYDHTLGRITLMAAMETNFGVGVVF--RN 419
DB 414 GSRMAWTLLEOGLGSGYKIGIYDSTKDDLSW--SKTDKIGGSPADOTVIKTFRELQ 472
OY 420 GERMGITKTFODFSREKVEKGEYNAVADTLEIINDTIRFQSGEPKDKTIILOELKISL 479
DB 473 KLFISVSLSLGIVLAVVCLSEFNINSHVRYIONSOPLNMLNLAAGSLAAVPLGL 532
OY 480 PLYSILSLALTLIGMTMAAFLEFNINKRNOKLIKMSPPYNNLILIGMLSYASIFLEGL 539
DB 533 DGYHIGRSOPPFVCOARLMLLGLGSLGSGMFTKIMWVHTVFTKKEEKKEMRKTLEPWK 592
OY 540 DGSFSEKTFETLCTVTRWMLTVGYTTAFGAMFAKTRVHAIF--KNVKMK--KRIIDOK 596
DB 593 LYATVGLVGMADVLTALWQVDPRLHRTIETFAKEEPKEDIVSILPOLEHSSKKMNTW 652
OY 597 LLVYVGMMLIDLCILICWQAVDPLRRTVEKYSMEPPDAGDISIRPLEHCENTHMTIW 656
DB 653 LGIFYGKGLLLGLIFLAYETKSVSTEKINDHRAVMAIYNAVLCITAPVTMILSQ 712
OY 657 LGIYAVYGLMLFGCFIAMETRNVSIPALNDSKTYIGMSVYNGIMCIIIGAVSFLTRDQ 716
DB 713 QDAAFAPASIAIVSSYITLVLFVPMKRLITRGE 748
OY 717 PNVQFCIVALVYIFCSTITLCLVFPVKLITLRTNPD 752

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RESULT 5
ID Q9WV15 PRELIMINARY; PRT; 833 AA.
AC Q9WV15;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, last sequence update)
DE 01-NOV-1999 (Tremblrel. 12, last annotation update)
DE 573K1.1.4 (GAMMA-AMINOBUTYRIC ACID (GABA) B RECEPTOR, ID).
GN 573K1.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC - Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA YOUNGER R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR - EMBL: AL078630; CAB44993.1; -.
KW Receptor.
SQ SEQUENCE 833 AA; 93167 MW; 0C07A359 CRC32;

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Query Match 24.5%; Score 1691; DB 11; Length 833;
 Best Local Similarity 35.4%; Pred. No. 0.00e+00;
 Matches 268; Conservative 194; Mismatches 271; Indels 23; Gaps 21;

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DB 2 GPGGCTPVGPRPLLVMAGVAPVMAWASHPLPRPRPRPPHSSERRAVYTGAL-FP 60
OY 11 GPPPPPPPPARLLLLLLPL-LPL-APGAMGWAQAPR-PP-PSSPPLSI-MGLMPLT 65
DB 61 MSGGWPQ-GQACOPAVEMALDVNSRDLDPDEYELKILHDSKCDPGQATYVELLYND 119
OY 66 KEVAKGSGRGLVLAPELAIEQIRNE-SLAPRYFLDLRLYTEDDNAGKGLKAFDAIKYG 124
DB 120 PIKIIIMFG-CSSVSTVLAEAARMNLIIVSYGSSPALSNRQRPPTFFRTHPSATLNP 178
OY 125 PNHLAVFEGVCPVSTSIASESLQGMNLVQLSFAATTPVLADKKRYPFERFVPSDANVP 184
DB 179 TRVLFKEMWKKIATIDQOTTEVFTSLDDLEERYKENGIFITRQSFSPAVPVNKL 238
OY 185 AILKILKYOMKRVGTLDQVDFSEVANDLTGLVLYGDEIDISTESFSDNPTCSVKKL 244
DB 239 RODARIIVGLFYEARKVCEVYKERLFGKKYVWFLIGWADWKF-KTY-DP-SINCTV 295
OY 245 GNDVRITILIGQFDQNMKAIVFCALDENNYGSKYMIIPGWTEFBSMWQVHTEANSKCLR 304
DB 296 EEMTEAVEGHITTEIVMLNPANTRISISNMTSQEFVEKLTTRKLHHPETGGFOEAPLAYD 355

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OY 305 KNLLAMEGYIGVDFEPLSSKQIKTISGTPQOY-BREYNN-KRSGVPSKH-G-YAED 360
DB 356 AIVALLALANKISG--GGRSGVRLDEPNYNNOTITDQIYRAMSSSEFGVGHVVDAS 413
OY 361 GIWIAKTLQRAMETLHASRHRQRIODFNYDHTLGRITLMAAMETNFGVGVVF--RN 419
DB 414 GSRMAWTLLEOGLGSGYKIGIYDSTKDDLSW--SKTDKIGGSPADOTVIKTFRELQ 472
OY 420 GERMGITKTFODFSREKVEKGEYNAVADTLEIINDTIRFQSGEPKDKTIILOELKISL 479
DB 473 KLFISVSLSLGIVLAVVCLSEFNINSHVRYIONSOPLNMLNLAAGSLAAVPLGL 532
OY 480 PLYSILSLALTLIGMTMAAFLEFNINKRNOKLIKMSPPYNNLILIGMLSYASIFLEGL 539
DB 533 DGYHIGRSOPPFVCOARLMLLGLGSLGSGMFTKIMWVHTVFTKKEEKKEMRKTLEPWK 592
OY 540 DGSFSEKTFETLCTVTRWMLTVGYTTAFGAMFAKTRVHAIF--KNVKMK--KRIIDOK 596
DB 593 LYATVGLVGMADVLTALWQVDPRLHRTIETFAKEEPKEDIVSILPOLEHSSKKMNTW 652
OY 597 LLVYVGMMLIDLCILICWQAVDPLRRTVEKYSMEPPDAGDISIRPLEHCENTHMTIW 656
DB 653 LGIFYGKGLLLGLIFLAYETKSVSTEKINDHRAVMAIYNAVLCITAPVTMILSQ 712
OY 657 LGIYAVYGLMLFGCFIAMETRNVSIPALNDSKTYIGMSVYNGIMCIIIGAVSFLTRDQ 716
DB 713 QDAAFAPASIAIVSSYITLVLFVPMKRLITRGE 748
OY 717 PNVQFCIVALVYIFCSTITLCLVFPVKLITLRTNPD 752

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RESULT 6
ID Q96022 PRELIMINARY; PRT; 844 AA.
AC Q96022;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, last annotation update)
DE GABAB RECEPTOR, SUBUNIT 1B, PRECURSOR.
DE GABAB-R1 OR GABA-B R1B OR GABBR1.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-CEREBELLUM;
RA WHITE J.H., WISE A., MAIN M.J., GREEN A., FRASER N.J., DISNEY G.H.,
RA BARNES A.A., EMSON P., FOORD S.M., MARSHALL F.H.;
RT "Heterodimerisation is required to form a functional GABAB receptor.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE-CEREBELLUM;
RA KAUPMANN K., SCHULDER V., MOSBACHER J., BISCHOFF S., BITTIGER H.,
RA HEID J., FROESTL W., LEONHARD S., PRAEF T., KARSCHIN A., BETTLER B.;
RT "Human gamma-aminobutyric acid type B receptors are differentially
RT expressed and regulate inwardly rectifying K+ channels.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:14991-14996(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA YOUNGER R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR - EMBL: AJ012186; CA009940.1; -.
DR - EMBL: AJ225029; CA012360.1; -.
DR - EMBL: AL031983; CA021454.1; -.
KW Signal; Receptor.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 844 GABAB RECEPTOR, SUBUNIT 1B.
SQ SEQUENCE 844 AA; 95148 MW; C7342B77 CRC32;

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Query Match 24.5%; Score 1695; DB 4; Length 844;
 Best Local Similarity 35.5%; Pred. No. 0.00e+00;
 Matches 255; Conservative 192; Mismatches 253; Indels 19; Gaps 17;


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[2]
RN SEQUENCE FROM N.A.
RP STRAIN-WISTAR.
RA PPAFF T., MALITSCHER B., KAUFMANN K., BETTLER B., KARSCHIN K.;
RT "Alternative splicing generates a novel isoform of the rat
   metabotropic GABAB receptor.";
RL Eur. J. Neurosci. 0:0-0(1999).
DR EMBL: Y10370; CAA71399.1; -.
DR EMBL: AF110797; AAD19657.1; -.
DR EMBL: AF110796; AAD19657.1; JOINED.
DR PIRAM; PF00003; 7tm_3; 1.
DR PIRAM; PF01094; ANF_receptor; 1.
RW Receptor.
SQ SEQUENCE 844 AA; 95037 MW; 6611P68D CRC32;

Query Match
Best Local Similarity 35.4%; Score 1690; DB 11; Length 844;
Matches 268; Conservative 194; Mismatches 271; Indels 23; Gaps 21;

Db 2 GPGGCPFPVGPPLPLLLVMAAGVAPVMAHSPHLPHPHPVPPPPSSRRVYVYIGAL-FP 60
Oy 11 GPPPPPPPPARLLLLLLPL-LPL-ARGAWGAKGAPR-PP-PSSPPPLSI-MGLMPLT 65
Db 61 MSGGMPG-GQACQPAVEMALEDVNSRRDILPDYELKLIHDSKCDPGQATKYELLYND 119
Oy 66 KEVAKGSIGRGVLPVAVELAIQIRNE-SILRPYFLDLRLYTECDNAKGLKAFYDAIKYG 124
Db 120 PKIILMPG-CSSSTIIVAEARMMNLIVLSYSSSPALSNROKPFPPFFRTHPSATLHP 178
Oy 125 PNHLMWGGVCPVSTIASELSQGNLVOLSFATTPVLADKKKYPFFFRTPSDNAVNP 184
Db 179 TRVLFKMGWKKIATIQOETEVSTLDDLEERKAGIEITRPSGSPDPAPVKNLK 238
Oy 185 AILKLKHKYKRGITLQDQKRSSEVRNDLTGLVGEDIEISDTESFSDPCSVAKKL 244
Db 239 RODARIIVGLFETEPARKVCEYTKERLFGKKYVWFLIGWADNWF-KTY-DP-SINCTV 295
Oy 245 GNDRIILIGFDQMAKAVFCACAEENMYGSKYOWIIPGWEPSPMQVHTEAMNSRCLR 304
Db 296 EEMTEAVGHTTEIIVMLNPNANTRISNMTSOEFVEKTRLRKHRETEGQEQAPLAYD 355
Oy 305 KNLLAAHEGTVGDPPEPLSSKQIKTISGKTPQOY-EREYNN-KRSGVPSKPFH-G-YAYD 360
Db 356 AIMALALALNKTSGG--GGRSGVRLIEDFNYNMOTITDOIYRAMNSSSFEVSGHYVDAS 413
Oy 361 GIWIAVIAKTLDRAVETLHASSRHOQIQDFNTDHTIGRIILMANNETNPFEGVIGQVVF-RN 419
Db 414 GSRMAWMLIBOLOGGSTKTKIGYDSTKDLSW-SKTDKWIIGSPPADQVLYITFRFLSQ 472
Oy 420 GERGMTKFTQFODSRREVKGVEYNAVADTLEIINDTIRFGSGSEPPKDKTILBQLKRISL 479
Db 473 KLFTSVLSLGIIVLAVVCLSFNIVSHRYIIONSPNLNLTAVCCSLAALAVPGLG 532
Oy 480 PLYITLALITLIGIMASAFLEFNINRNOCKLLKMSSPYNNLITLIGMISYSLFGL 539
Db 533 DGHIGHSGEPFVCOARLMLGLGSLGYSMTKIMWVTVFTKKEEKEMKTELEPMK 592
Oy 540 DGSPVSEKTEFETLCTVETLITGYTTAFGAMFAKTMRVHAIF--KNVMK-KKIIKDK 596
Db 593 LKATVGLVGMVDVLTIAIWOIVDPLHRTITETFAKEPKEDIVSILPOLHSSSKMNTW 652
Oy 597 LVIYVGMGLIDICILICQWQAVDPLRRTVEKYSMEPPDAGRIDISIRPLEHCENHTMTW 656
Db 653 LGIFYGKGLLLGLIFLAETKSYSTEKINDHRAVGMATYNAVYCLITAPYTMILSSQ 712
Oy 657 LGIYVAKGLMLFGCLAMETKNSIPALNDSKYIGMSYVNVGIMCIIGAAYSFLTRDQ 716
Db 713 QDAAFASLAIVSSYITLVLEVFKMRRLITRGE 748
Oy 717 PNVOFCIVALVITFCSTITLCTVFPVKLITLRINPD 752

RESULT 9
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ID 095975 PRELIMINARY; PRT; 899 AA.
AC 095975;
DT 01-MAY-1999 (TREMBLrel, 10, Created)
DT 01-MAY-1999 (TREMBLrel, 10, last sequence update)
DT 01-MAY-1999 (TREMBLrel, 10, last annotation update)
DE GABAB RECEPTOR, SUBUNIT 1C PRECURSOR.
GN GABAB-R1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RA WHITE J.H., WISE A., MAIN M.J., GREEN A., FRASER N.J., DISNEY G.H.,
RA BARNES A.A., EMSON P., FOORD S.M., MARSHALL F.H.;
RT "Heterodimerisation is required to form a functional GABAB receptor.";
RL Submitted (OCU-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; A012187; CAA09941.1; -.
KW Signal; Receptor.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 899 GABAB RECEPTOR, SUBUNIT 1C.
SQ SEQUENCE 899 AA; 101551 MW; 04619FDC CRC32;

Query Match
Best Local Similarity 36.2%; Score 1687; DB 4; Length 899;
Matches 249; Conservative 180; Mismatches 243; Indels 16; Gaps 14;

Db 123 GQACQPAVEMALEDVNSRRDILPDYELKLIHDSKCDPGQATKYELLYNDPKIILMP 182
Oy 74 GRGVLPAVELAIQIRNE-SILRPYFLDLRLYTECDNAKGLKAFYDAIKGPNHLMWFG 132
Db 183 G-CSSSTIIVAEARMMNLIVLSYSSSPALSNROKPFPPFFRTHPSATLHPTRYKLEK 241
Oy 133 GVCPSVSTIIASLQGNLVOLSFATTPVLADKKKYPFFFRTPSDNAVNPAILKLKH 192
Db 242 WGWKKIATIQOETEVSTLDDLEERKAGIEITRPSGSPDPAPVKNLKRODARIIV 301
Oy 193 YOKKRGITLQDQKRSSEVRNDLTGLVGEDIEISDTESFSDPCSVAKKLGNQVRIIL 252
Db 302 GLPYETEARVCEYTKERLFGKKYVWFLIGWADNWF-KTY-DP-SINCTVDENTEAVE 358
Oy 253 GQFDQMAKAVFCACAEENMYGSKYOWIIPGWEPSPMQVHTEAMNSRCLRKNLLAME 312
Db 359 GHTEIIVMLNPNANTRISNMTSOEFVEKTRLRKHRETEGQEQAPLAYDAIMALALA 418
Oy 313 GTIGVDEPLSSKQIKTISGKTPQOY-EREYNN-KRSGVPSKPFH-G-YAYDGIWIAVIAKT 368
Db 419 LNKTSGG--GGRSGVRLIEDFNYNMOTITDOIYRAMNSSSFEVSGHYVDASGSRMAWTL 476
Oy 369 LQRAVETLHASSRHOQIQDFNTDHTIGRIILMANNETNPFEGVIGQVVF-RNGERMGITK 427
Db 477 IDOLOGGSTKTKIGYDSTKDLSW-SKTDKWIIGSPPADQVLYITFRFLSQKLFISVS 535
Oy 428 FTQFODSRREVKGVEYNAVADTLEIINDTIRFGSGSEPPKDKTILBQLKISL 487
Db 536 LSLIGIIVLAVVCLSFNIVSHRYIIONSPNLNLTAVCCSLAALAVPGLDGYHIGRN 595
Oy 488 LTIIDGIMASAFLEFNINRNOCKLLKMSSPYNNLITLIGMISYSLFGLIDSPVSEK 547
Db 596 QEPFVCOARLMLGLGSLGYSMTKIMWVTVFTKKEEKEMKTELEPMKLAATAGL 655
Oy 548 TPEITCTYRTMLITGYTTAFGAMFAKTMRVHAIF--KNVMK-KKIIKDKLVIYVGM 604
Db 656 VGMVDVLTIAIWOIVDPLHRTITETFAKEPKEDIVSILPOLHSSSKMNTWLGTFYGYK 715
Oy 605 LIIDICILICQWQAVDPLRRTVEKYSMEPPDAGRIDISIRPLEHCENHTMTWIGIYAYK 664
Db 716 GLIILGIFLAETKSYSTEKINDHRAVGMATYNAVYCLITAPYTMILSSQDAAFAPA 775
Oy 665 GLIMLEGGFLAMEWTRNYSIPALNDSKYIGMSYVNVGIMCIIGAAYSFLTRDQPNVOFCIV 724
Db 776 SLATVSSYITLVLEVFKMRRLITRGE 803
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Oy	74	GRGVLPAAVEALAEIQIRNE - SLIRPEFDLRLYTEDCNKKGAKAFDAIKYCPNHLWFG	132
Db	244	G-CSSSTTVAIAAAMNMLIYLSTGSSSPALSROFPPEFPHPSATLHNPTRYKLEK	302
Oy	133	GVCPSSTTITASLOGNNLVLSFATTPALDOKKPYFPFRTVSDNAVPAIKLKLKH	192
Db	303	WGKKIATITIOOTTEVFSTLDDLEERKKEIGETITROSFPSPAPVKNLRODARTIV	362
Oy	193	YOMKRVGLTDOVORFSEVRNDLGVLYGDEIDESTESNDPCYSKKLKGNDVIRIL	252
Db	363	GLVEFEARVCEYKKEKRLGKKYKVFLLIGWADMF - KTY-DP-SICUYEETKAVE	419
Oy	253	GEPDQMAAKVCCAYEENMYGSKYOMITPGVYEPSMEQVHTEANSRCKRLNLAME	312
Db	420	GHTTETIVMLNANTRISNMNTSOEPEKLTKLKLRHPEGTGFOEARLAVDAIYALALA	479
Oy	313	GYGVGFPELSSKQIKITISGTPQOY - EREYN - KNSGVGFSKFH - G - YADGIVIAKTI	368
Db	480	LNTSGG - GGRSGVLEDFVYNNOTITDOIYRAMNSSFEGVSGHYVFDASGSHMAVTL	537
Oy	369	LORAMETLHASSRHORIDDFNYTDHTLGRILILNANMETNFEVGTGVVF - RNCERMGYIK	427
Db	538	IELOGYSKKICYDSTPKDDLW - STDWKMGSPADOTLVTKFRRLSOKLEISVS	596
Oy	428	FTPQDSREVKYGEVNAVAADLEIINOTIRQSEPPKOKITILBQLRKISLPLYSILSA	487
Db	597	LSSLGIYLAIVCLSNRYNSHAKYIONSOPRLNLTNRAVCSALAVPFLGIDGTHIGRS	656
Oy	488	LTLGIMKASAPLEPYNINRNOKLIKSSPPMNNLLIGMISTASYATFLFGDSFSEK	547
Db	657	QPPFVCOARLMLGLGFSIGVSMETRIKWVHVYTKKEKKEMKRLTPMKLYATVGLL	716
Oy	548	TEFLCTVPTWMLITGVYTTAGCAFEATWVRHALF - KVKMK - KKLIDOKKLYIVGGM	604
Db	717	VGADVLTLLIMQIYVRLRTIETFAKEPKREDIVSTIPLOLESCKSKMNTLGIIFYGX	776
Oy	605	LILDCLILCOMANDPLRYKTEKSMEDDAGRDRISIRPLBHCENTHMTIMLGIVAYKK	664
Db	777	GLLLIGITLAYETKSVSTEKINDHRAVGMATYVAVLCLITAPVTMLISSODAPAFYA	836
Oy	665	GLMLRGCLPLMETRNVSPALNDSKTYIGMSVYVNGIMCIGAAVSFLTRDOPNVQFCIV	724
Db	837	SLATVFSYITLVVLFPVKMRLLTRGE	864
Oy	725	ALVITFCSTLCLVFPRLTLRTNPD	752
RESULT	15		
ID	Q9WV16	PRELIMINARY:	PRT: 662 AA.
AC	Q9WV16;		
DT	01-NOV-1999 (TREMBLrel. 12, Created)		
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)		
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)		
DE	573K1.1.3 (GAMMA-AMINO BUTYRIC ACID (GABA) B RECEPTOR, 1c).		
EN	573K1.1.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	YOUNGER R.;		
RL	Submitted (May-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AL078630; CAB44992.1; -.		
KW	Receptor.		
SQ	SEQUENCE 662 AA: 74593 MW; 3B469368 CRC32;		
Query Match	19.7%;	Score 1360;	DB 11; Length 662;
Best Local Similarity	33.9%;	Pred. No. 2,18e-749;	
Matches	226; Conservative 172;	Mismatches 246;	Indels 23; Gaps 21.
Oy	2	GGGCGCTPGVGLPRLILYMAAGVAPWASHSPHLPKPHVPRVPHPSSEKRAYITAL-PP	60
Oy	11	GGPPPPPPARLILLLILPL-LPLP-ARGGWMGAKGAP-PP-PSSPPLST-MGLMPLT	65

Sun Apr 23 09:55:05 2000

US-09-211-755A-47.rsp

Page 10

Dp	61	MSGWGC -GOCAPVMEALNDVNSRDIIDPDELKIHNSCOPGATVTELLYND	119
Qy	66	KEVAKSISGRVLPVAVELAIQIRNE -SLRPFLDLRLYTECONMAGLKAFDAIKYG	124
Dp	120	PIKIIIMPQ -CSSVSTLVAEARMMNLVLSTOSSSPALSNQRPPTFRPHSATLNP	178
Qy	125	PNHLVFGVGSVYSIISAELOSQMIVOLSFAPATTPVLADKKPYFFRFRVPSDANVP	194
Dp	179	TRYKLEKGMWKIATIOQTTEVSTPLDLEERVAEAGIETFPQSEFSDPAPVANKL	238
Qy	185	AIILKIKHYOMKRVGTLLQDQRESEVRNLDLTVGLGEDIEISDPESNDPCHSVAKK	244
Dp	239	ROARIIYGLFVETBARVPECVYKEBFGKYYVWFLIGMYADNMF -KTY -DP -SINCY	295
Qy	245	GNQVRILLIQFOQNNAAKVPCCAEENNYOSKQIIPOMTERSWMEOVHTEAUSSCLR	304
Dp	296	EEMTEAVEGHITTEIYMLNPANTRTSISNMTSOEFVEKLYRKLRPDESTGFOBPALYD	355
Qy	305	KNLIAAMEGYIVDEPRLSSQOITIGSKTPQOY -BREYVN -KRSQVSPSKFH -G -YAYD	360
Dp	356	AIMALALNKRSGG -GGRSGVRLPEFPNNNOITIDOLYRAAMNSSPEGSGVHYVDAS	413
Qy	361	GIWIVAKTIQRAMETLIHSSRQRIQDPNTDHTLGRILNMAENETNFGYTGQVFE -RN	419
Dp	414	GSRMANLTLEOLQSGSYKKIIGYDSTKXDLISW -SKTDNMIGSSPPADOTIVIKTFRLSQ	472
Qy	420	GERMGITKFTFOQDREKVEYENAVADLEIINDIRFQSGSEPKDXTIILBOLRISL	479
Dp	473	KLFJASVYSSJGIYLAUVCSFNPNYSHRVYIONSOPNINMLTVAGSILMAAVFPLGL	532
Qy	480	PVSIISALTILGIMIAASFLEFPIKNRPNQKLIKMSPPYMNNDIILGMLYASIFPLGL	539
Dp	533	DGHHIGRSQFPVCOARMLLGLGFSJLGSYMTKTIWNYHIVYTKKEKKEKMKRTLEPMK	592
Qy	540	DGSFSEKFFELCTVIRWMLTVGTYTAFGAMEPAKTRVNAHF -KNVKKM -KPIIDOK	596
Dp	593	LYATVGLGMDILTLATIQVLDIPIHRTITFKAKEPEKEDIVSLIPOLERSSKKNMTY	652
Qy	597	LTVIVGMLLIDICILGQAVDAPLRKTRVEKSNEDPAGRIDISIRPLLECENHTMTIW	656
Dp	653	LGELMSF 659	
Qy	657	LGIVYAY 663	

Search completed: Wed Apr 19 22:06:59 2000
Job time : 679 secs.

FT	CHAIN	34	908	EXTRACELLULAR GLUTAMATE RECEPTOR 8.
FT	DOMAIN	34	583	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	584	608	I (POTENTIAL).
FT	DOMAIN	609	620	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	621	641	II (POTENTIAL).
FT	DOMAIN	642	647	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	648	668	III (POTENTIAL).
FT	DOMAIN	669	695	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	696	716	IV (POTENTIAL).
FT	DOMAIN	717	746	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	747	768	V (POTENTIAL).
FT	DOMAIN	769	781	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	782	803	VI (POTENTIAL).
FT	DOMAIN	804	818	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	819	843	VII (POTENTIAL).
FT	DOMAIN	844	908	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	95	298	POTENTIAL.
FT	CARBOHYD	298	452	POTENTIAL.
FT	CARBOHYD	452	480	POTENTIAL.
FT	CARBOHYD	480	565	POTENTIAL.
SO	SEQUENCE	908 AA;	101413 MM;	255B10FP CRC32;
Query Match		3.5%;	Score 241;	DB 1;
Best Local Similarity		22.1%;	Pred. No. 2.6e-20;	Length 908;
Matches	64;	Conservative	99;	Mismatches 101;
				Indels 25;
				Gaps 22.
Db	584	AVPPLVLAIIIGI-ATTFVIVTFVFRYNDPPIVRSAGRLSVLLTGIFLCISYFLM-I-	640	
Oy	483	SILSL-ITLIGIMASAPLFPN-INKNRQKLIKMSPPMNNLLILGMLVSAISFLFGLD	540	
Db	641	AA--PD-TI--ICSFRIIFLGKMCFSYALLTNTNRHFRFEQGSVTPAKTISPAQ	695	
Oy	541	GSFVSEKTFEPFLCVFRTWTLFVGYTATGAFMFAKTRVHALEFKVKKM-K--KIHKQKL	597	
Db	696	LYTFEFLSVOLLGVEFVVDP--PHTIIDG-EGORTDPE-NARGVLR-CDISDLSL-I	750	
Oy	598	LYIVAGMLLIDCLICQANDPLRLRYTEKXSMEDPAGRIDISIRPLDHEGNHTMTWL	657	
Db	751	CSL-GYSILMW-TC-TVYAIKTRGVPETENAPKIGFTMYTTCIIMLAFPIFFGAQS	807	
Oy	658	GIVYAVKGLHMGFCFLAMETRNWSIP-ALNDSKYGISVAVGIMCIGAAVSFLRDSQ	716	
Db	808	AEKMTIQTTLTVLSMSLSASVSLGLVMPKYIIIFHEQUNOKRSKF	856	
Oy	717	PWVQFC-IVALVI-I-FCSITLCLVFPKLTITLTPDAATONRRPQF	762	
RESULT	2	STANDARD:	PRF:	871 AA.
ID	MGRE RAT			
AC	P35349;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	15-JUN-1999 (Rel. 38, Last annotation update)			
DE	METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.			
GN	GRM6 OR MGJUR6.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=RETINA;			
RX	MEDLINE: 93280152.			
RA	NAKAJIMA Y., IWAKABE H., AKAZAWA C., NAWA H., SHIGEMOTO R.,			
RA	NAKAMISHI S.,			
RT	"Molecular characterization of a novel retinal metabotropic glutamate			
RT	receptor mGluR6 with a high agonist selectivity for L-2-amino-4-			
RT	phosphonobutylate.";			
RL	J. Biol. Chem. 268:11868-11873(1993).			
CC	-1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR			
CC	IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE			
CC	ACTIVITY.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			

[illegible]

AC P70579;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
 GN GRM8 OR MGLUR8.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97168760.
 RA SAUSTAD J.A., KINZIE J.M., SHINOHARA M.M., SEGGERSON T.P.,
 RA WESTBROOK G.L.;
 RT "Cloning and expression of rat metabotropic glutamate receptor 8
 RT reveals a distinct pharmacological profile."
 RL Mol. Pharmacol. 51:119-125(1997).
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
 CC ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: PROMINENT EXPRESSION IN OLFACTORY BULB,
 CC PONTINE GRAY, LATERAL RETICULAR NUCLEUS OF THE THALAMUS, AND
 CC PIRIFORM CORTEX. LESS ABUNDANT EXPRESSION IN CEREBRAL CORTEX,
 CC HIPPOCAMPUS, CEREBELLUM, AND MAMMARY BODY.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL: U63288; AAB09537.1; -;
 CC DR GCRDB: GCR.1411; -;
 CC DR PROSITE: PS00979; G_PROTEIN_REC_P3_1; 1;
 CC DR PROSITE: PS00980; G_PROTEIN_REC_P3_2; 1;
 CC DR PROSITE: PS00981; G_PROTEIN_REC_P3_3; 1;
 CC DR PFAM: PF01094; ANF_receptor; 1;
 CC DR PFAM: PF01094; ANF_receptor; 1;
 CC DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 CC Multigene family; Olfaction.
 CC FT SIGNAL 1 33
 CC FT CHAIN 34 908
 CC FT DOMAIN 34 583
 CC FT TRANSMEM 584 608
 CC FT DOMAIN 609 620
 CC FT TRANSMEM 621 641
 CC FT DOMAIN 642 647
 CC FT TRANSMEM 648 668
 CC FT DOMAIN 669 695
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 CC FT DOMAIN 769 781
 CC FT TRANSMEM 782 803
 CC FT DOMAIN 804 818
 CC FT TRANSMEM 819 843
 CC FT DOMAIN 844 908
 CC FT CARBOHYD 95 95
 CC FT CARBOHYD 298 298
 CC FT CARBOHYD 452 452
 CC FT CARBOHYD 480 480
 CC FT CARBOHYD 565 565
 CC FT SEQUENCE 908 AA; 101866 MW; 5043PF81 CRC32;
 DB 590 IATLGI-ATTEVIVTAVRNDTPIVRASGRSLVLTGFLCYSTPLM-I-AA--PD 644

Query Match 3.4%; Score 237; DB 1; Length 908;
 Best Local Similarity 22.3%; Pred. No. 1,286-19;
 Matches 63; Conservative 96; Mismatches 100; Indels 24; Gaps 21;
 DB 590 IATLGI-ATTEVIVTAVRNDTPIVRASGRSLVLTGFLCYSTPLM-I-AA--PD 644

488 IITLIGMTMSAFLFFN-INNRNOKLIMSSPYMNNLITLIGMGLASVIFGLGSPVSE 546
 645 -TI-ICSFRIPLGLMCESTAAITLTKNRHIFEDGKSVTAAPRISASVLTTFES 701
 547 KTFELCTVETWVILVGYTGAAGAMAKTWALFKVKKR-K-KIKOQKLLVTVG 603
 702 LISVOLLGVVWVVDV-PHTIIDP-EDRTIDPE-NARGVYK-CDISDLSL-ICSL-GV 755
 604 MLIDLCILICWADVPLRRTVEKISMEDPPAGRISIRPLEHCENTHMTWIGIYAY 663
 756 SILLV-TC-TYVAITKGVPTFNKAPIGFTWYTCIIMLAFIPFGTAQSAERWYI 813
 664 KGLIMLEGCFLAMETNNVSI-P-ALNDISKYIGMSYVNVGIMCIGAAVSFLTRDPNVQFC 722
 814 OTTLITVMSLSASVSLGMLYMPKYIILFHEDQVVKRKSF 856
 723 -YVALVI-I-FCSTYTLCLVFPKLTITLTPDAAVNNRRPF 762

RESULT 4
 ID MGR8_HUMAN STANDARD; PRT; 908 AA.
 AC 000222; 015493;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
 GN GRM8 OR MGLUR8.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98141892.
 RA WU S., WRIGHT R.A., ROCKEY P.K., BURGESS S.G., ARNOLD J.S.,
 RA POSTECK P.R., JR., JOHNSON B.G., SCHORPP D.D., BELAGAJE R.M.;
 RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
 RT pharmacological cloning, functional expression, and comparison of
 RT pharmacological properties in RGT cells."
 RL Brain Res. Mol. Brain Res. 53:88-97(1998).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC MEDLINE: 97446143.
 CC SCHERRER S., SODER S., DUVOISIN R.M., HUIZENGA J.J., TSUI L.C.;
 RA "The human metabotropic glutamate receptor 8 (GRM8) gene: a
 RT disproportionately large gene located at 7q31.3-q32.1."
 RL Genomics 44:232-236(1997).
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
 CC ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL: U92459; AAB51764.1; -;
 CC DR EMBL: U95025; AAB72040.1; -;
 CC DR GCRDB: GCR.1889; -;
 CC DR GCRDB: GCR.2604; -;
 CC DR MIM: 601116; -;
 CC DR PROSITE: PS00979; G_PROTEIN_REC_P3_1; 1;
 CC DR PROSITE: PS00980; G_PROTEIN_REC_P3_2; 1;
 CC DR PROSITE: PS00981; G_PROTEIN_REC_P3_3; 1;
 CC DR PFAM: PF01094; ANF_receptor; 1;
 CC DR PFAM: PF01094; ANF_receptor; 1;
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 CC Multigene family; Olfaction.

```

FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR 8.
FT DOMAIN 34 583 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 584 608 I (POTENTIAL).
FT DOMAIN 609 620 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 621 641 II (POTENTIAL).
FT DOMAIN 642 647 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 648 668 III (POTENTIAL).
FT DOMAIN 669 695 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 696 716 IV (POTENTIAL).
FT DOMAIN 717 746 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 747 768 V (POTENTIAL).
FT DOMAIN 769 781 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 782 803 VI (POTENTIAL).
FT DOMAIN 804 818 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 819 843 VII (POTENTIAL).
FT DOMAIN 844 908 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 POTENTIAL.
FT CARBOHYD 298 298 POTENTIAL.
FT CARBOHYD 452 452 POTENTIAL.
FT CARBOHYD 480 480 POTENTIAL.
FT CARBOHYD 565 565 POTENTIAL.
FT CONFLICT 194 194 R -> A (IN REF. 2).
FT CONFLICT 460 460 T -> I (IN REF. 2).
FT CONFLICT 642 642 A -> G (IN REF. 2).
FT CONFLICT 768 768 N -> I (IN REF. 2).
FT CONFLICT 904 904 S -> T (IN REF. 2).
SQ SEQUENCE 908 AA: 101741 MM: 18865CQF CRC32:

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Query Match 3.4%; Score 232; DB 1; Length 908;

Best Local Similarity 23.0%; Pred. No. 9,25e-19; Mismatches 98; Indels 24; Gaps 21;

Matches 65; Conservative

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Db 590 VALIGII-ATTFYIVFVRNDPIYRASGRELSTYVLGIFLCYSITPLM-I-AA--PD 644
QY 488 LITLIGIMASAFLEFN-IKRNQKLIKMSPPYNNLLIIGMLSTASIFLFGDGSFVEB 546
Db 645 -TT--TCSFRRVLGLCMSTYALTKTRIRIRIFEOGKSKSTAKFISPAQIVITFS 701
QY 547 KTFETLTCTVETWILVGYTTAFGMAFKTRVHAIFKNVKK-K-KIKDKQLVIYVG 603
Db 702 LISVOLLGVFVFWVDPEHIID-YG-EQRTLDPEKA-RGVLK-CDISDLSL-IGSL-GY 755
QY 604 MLTIDLCILICWQAVDPLRKTVEKSMRPPADGRDISIRLLEHCENTHMTWLGIVYV 663
Db 756 SILIMTC-TCTVYANKTRGV-ETFNEAKPIGFTWYTCIILAFPIFFGTAQSAEKMT 813
QY 664 KGLMLFGCFL-AMETRNVSIPALNDSKYIGMSYVNGIMCIIGAAVSFLTRDPNVQFC 722
Db 814 QTTTLVMSLSASVSGLMLYPRVYIIIFHPEDNQOKRRSF 856
QY 723 -YVALVI-I-FCSITTLCLVFPRLTLRTNPDAATQNRROF 762

```

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RESULT 5 STANDARD; PRT; 877 AA.
ID MGR6_HUMAN
AC 015303;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.
GN GRM6 OR MGLUR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE; 97358610.
RA HASHIMOTO T., INAZAWA J., OKAMOTO N., TAGAMA Y., BESSHO Y., HONDA Y.,
RA NAKANISHI S.:
RT "The whole nucleotide sequence and chromosomal localization of the
RT gene for human metabotropic glutamate receptor subtype 6."
RL Eur. J. Neurosci. 9:1226-1235(1997).

```

```

CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR4.
CC -----
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CC OR SEND AN EMAIL TO license@isb-sib.ch).
CC -----
DR EMBL; U82083; AAB82068.1; -.
DR GCDR; GCR_2607; -.
DR MIM; 604096; -.
DR PROSITE; PS00979; G-PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G-PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G-PROTEIN_RECEP_F3_3; 1.
DR PFAM; PF00003; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Vision.
FT SIGNAL 1 24
FT CHAIN 25 877
FT DOMAIN 25 585
FT TRANSMEM 586 608
FT TRANSMEM 609 622
FT TRANSMEM 623 643
FT TRANSMEM 644 654
FT TRANSMEM 655 673
FT TRANSMEM 674 697
FT TRANSMEM 698 718
FT TRANSMEM 719 748
FT TRANSMEM 749 770
FT TRANSMEM 771 783
FT TRANSMEM 807 819
FT TRANSMEM 820 845
FT TRANSMEM 846 877
FT DOMAIN 878 897
FT CARBOHYD 296 296
FT CARBOHYD 451 451
FT CARBOHYD 479 479
FT CARBOHYD 567 567
SQ SEQUENCE 877 AA: 95436 MM: D5A6C038 CRC32:

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Query Match 3.3%; Score 225; DB 1; Length 877;

Best Local Similarity 21.5%; Pred. No. 1.44e-17; Mismatches 106; Indels 22; Gaps 19;

Matches 60; Conservative

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Db 592 LAVLGIVATTVVAFVRNNTPIYRASGRELSTYVLGIFLIVY-I-TF-L---MVAEP 645
QY 488 LITLIGIMASAFLEFN-IKRNQKLIKMSPPYNNLLIIGMLSTASIFLFGDGSFVEB 547
Db 646 G-AAVCAARRFLGLGTTTSYALTKTRIRYIFEOGKRSVTPPFISSQIVITFSL 704
QY 548 TTEETLTCTVETWILVGYTTAFGMAFKTRVHAIFKNV-K-KKR-IKDKQLVIYVGM 604
Db 705 TSLQVGMATMGARPHSVID-YE-EQRTVDEQA-RGVLK-CMDSLSL-IGSL-GY- 757
QY 605 ILTIDLCILICWQAVDPLRKTVEKSMRPPADGRDISIRLLEHCENTHMTWLGIVYV 664
Db 758 SILIMTC-TVAIKARGVPETFEAKPIGFTWYTCIILAFVPIFFGTAQSAEKIYQ 816
QY 665 GLTMLFGCFLAMETRNVSIP-ALNDSKYIGMSYVNGIMCIIGAAVSFLTRDPNVQFC- 722
Db 817 TTTTLVMSLSASVSGLMLYPRVYIIIFHPEDNQOKRR 855
QY 723 YVALVI-I-FCSITTLCLVFPRLTLRTNPDAATQNR 759

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RESULT	6	STANDARD:	PRT:	912 AA.
ID	MGRA_HUMAN			
AC	Q14833;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-DEC-1999 (Rel. 39, Last annotation update)			
DE	METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.			
GN	GRM4 OR MGLU4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
RC	[1]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE-BRAIN:			
RA	MAAOFF A., LEICHHUK R., OXER M., HARRINGTON K., EMSON P.:			
RT	"Molecular characterization and localization of human metabotropic glutamate receptor type 4."			
RL	Brain Res. Mol. Brain Res. 37:239-248(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 98141892.			
RA	WU S., WRIGHT J.R., ROCKEY P.K., BURGETT S.G., ARNOLD J.S.,			
RT	ROSTECK P. R., JR., JOHNSON B.G., SCHOEPP D.D., BELGAARD R.M.:			
RL	"Group III human metabotropic glutamate receptors 4, 7 and 8: molecular cloning, functional expression, and comparison of pharmacological properties in RGT cells."			
RN	Brain Res. Mol. Brain Res. 53:88-97(1998).			
RP	[3]			
RC-	SEQUENCE FROM N.A.			
RX	TISSUE-BRAIN:			
RA	MEDLINE: 95342351.			
RT	FLOR P.J., LUKIC S., RUEEGG D., LEONHARDT T., KNOEPFEL T., KUHN R.:			
RL	"Molecular cloning, functional expression and pharmacological characterization of the human metabotropic glutamate receptor type 4."			
CC	Neuropharmacology 34:149-155(1995).			
CC	-1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN THE CEREBELLUM, EXPRESSED AT LOW LEVELS IN HIPPOCAMPUS, HYPOTHALAMUS AND THALAMUS. NO EXPRESSION DETECTED IN LIVER.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS. STRONGEST TO MGLUR6.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: X80818; CAA56784.1; -			
DR	EMBL: U92457; AAB51762.1; -			
DR	GCRDB: GCR_1891; -			
DR	GCRDB: GCR_2069; -			
DR	MIM: 604100; -			
DR	PROSITE: PS00979; G_PROTEIN_REC_P_F3_1; 1.			
DR	PROSITE: PS00980; G_PROTEIN_REC_P_F3_2; 1.			
DR	PROSITE: PS00981; G_PROTEIN_REC_P_F3_3; 1.			
DR	PFAM: PF00003; 7tm_3; 1.			
DR	PFAM: PF01094; ANF_receptor; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;			
KW	Multigene family.			
FT	SIGNAL	1	32	POTENTIAL.
FT	CHAIN	33	912	METABOTROPIC GLUTAMATE RECEPTOR 4.
FT	DOMAIN	33	587	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	588	610	I (POTENTIAL).
FT	DOMAIN	611	624	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	625	645	II (POTENTIAL).

FT	DOMAIN	646	656	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	657	675	III (POTENTIAL).
FT	DOMAIN	676	699	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	700	720	IV (POTENTIAL).
FT	DOMAIN	721	750	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	751	772	V (POTENTIAL).
FT	DOMAIN	773	785	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	786	808	VI (POTENTIAL).
FT	DOMAIN	809	821	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	822	847	VII (POTENTIAL).
FT	DOMAIN	848	912	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	98	98	POTENTIAL.
FT	CARBOHYD	301	301	POTENTIAL.
FT	CARBOHYD	454	454	POTENTIAL.
FT	CARBOHYD	484	484	POTENTIAL.
FT	CARBOHYD	569	569	POTENTIAL.
SQ	SEQUENCE	912 AA;	101867 MW; 74009054 CRC32;	
Query Match 3.3%; Score 228; DB 1; Length 912;				
Best Local Similarity 21.6%; Pred. No. 4.46e-18;				
Matches	62; Conservative	98; Mismatches	100; Indels	27; Gaps
Db	588	AVLPPLFLAVWG-IATLTFVVTFRYNDTPVKASGRELSTVLLAGIFLCYATFTL-M-6433		
Qy	483	SILSR-LTILIGIMASALFLPN-IKNRQKIKKSSPYMMNLILIGLMSLYASFLFGLD-5400		
Db	644	--IAEPDLGT-CSLRIETLIGISISYALLTKNRIRYIEFGKRSVASPREISPASQ-6599		
Qy	541	GSEVSEKTEFTLCTVETWILTVGYTTAFAMFAKTRWHALFKNVK--MKK-KIKDOKL-5978		
Db	700	LAITFSLISDGL-IGICWFPVVDPSHSVD-FQDQRLDHR-FA-RGVLR-CDISDLSL-7533		
Qy	598	LVIYGGMLIDLCILIC-WQAVDPLRLRVEKYSNEPPDAGDISIRPLEHCENTHWTIW-6566		
Db	754	ICLL-GYSMLMW-TC-TVAIAIKRGVDEPENEKPIGFMTYTCIYWLAFIPIFGTSQ-8100		
Qy	657	LGIYVAYGLMLTGCCFLAMETRVNSIP-ALNDSKRYIGMSYVNWGICITGAANSFLTRD-7155		
Db	811	SADKLIYQTTTLTWSVLSASVSIGMLYMPKVIYIILFHPPEONPKRK-857		
Qy	716	QPNVQFC-IYALVLI-I-PCSTITLCIYVPRLLILRLNPDQAQGNRR-759		
RESULT	7			
ID	MGR4_RAT	STANDARD;	PRT;	912 AA.
AC	P31423:			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.			
GN	GRM4 OR MGLD4.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN;			
RX	MEDLINE: 92110002.			
RA	TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKAMISHI S.;			
RT	"A family of metabotropic glutamate receptors.";			
RL	Neuron 8:169-179(1992).			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN;			
RX	MEDLINE: 93332699.			
RA	O'HARA P.J., SHEPPARD P.O., THOGERSEN H., VENEZIA D., HALDEMAN B.A.,			
RA	MCGRANE V., HOUNEED K.M., THOMSEN C., GILBERT T.L., MULVATHILL E.R.;			
RT	"The ligand-binding domain in metabotropic glutamate receptors is			
RT	related to bacterial periplasmic binding proteins.";			
RL	Neuron 11:41-52(1993).			
CC	-I- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR			
CC	IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE			
CC	ACTIVITY.			


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CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT
CC EXPRESSION IS SEEN IN THE GRANULE CELLS OF THE CEREBELLUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR6.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC CC
CC EMBL: M92077; -; NOT ANNOTATED_CDS.
CC EMBL: M90518; AAA93190.1; -.
CC PIR: JH0563; JH0563.
CC GCRDB: GCR_0352; -.
CC DR GCRDB: GCR_0352; -.
CC DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
CC DR PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
CC DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
CC DR PFAM: PF00003; 7tm_3; 1.
CC DR PFAM: PF01094; ANF_receptor; 1.
CC DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC Multi-gene family.
CC KW SIGNAL
CC FT CHAIN 1 32 POTENTIAL.
CC FT DOMAIN 33 912 METABOTROPIC GLUTAMATE RECEPTOR 4.
CC FT TRANSSEM 33 587 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 588 610 I (POTENTIAL).
CC FT TRANSSEM 611 624 CYTOPLASMIC (POTENTIAL).
CC FT TRANSSEM 625 645 II (POTENTIAL).
CC FT DOMAIN 646 656 EXTRACELLULAR (POTENTIAL).
CC FT TRANSSEM 657 675 III (POTENTIAL).
CC FT TRANSSEM 676 699 CYTOPLASMIC (POTENTIAL).
CC FT TRANSSEM 700 720 IV (POTENTIAL).
CC FT TRANSSEM 721 750 EXTRACELLULAR (POTENTIAL).
CC FT TRANSSEM 751 772 V (POTENTIAL).
CC FT TRANSSEM 773 785 CYTOPLASMIC (POTENTIAL).
CC FT TRANSSEM 786 808 VI (POTENTIAL).
CC FT TRANSSEM 809 821 EXTRACELLULAR (POTENTIAL).
CC FT TRANSSEM 822 847 VII (POTENTIAL).
CC FT TRANSSEM 848 912 CYTOPLASMIC (POTENTIAL).
CC FT TRANSSEM 98 98 POTENTIAL.
CC FT CARBOHYD 301 301 POTENTIAL.
CC FT CARBOHYD 454 454 POTENTIAL.
CC FT CARBOHYD 484 484 POTENTIAL.
CC FT CARBOHYD 569 569 POTENTIAL.
CC FT CONFLICT 124 124 Q -> R (IN REF. 2).
CC SQ SEQUENCE 912 AA; 101818 MW; 95FE3E7D6 CRC32;

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Query Match 3.3%; Score 225; DR 1; Length 912;
 Best Local Similarity 22.6%; Pred. No. 1,44e-17;
 Matches 65; Conservative 93; Mismatches 101; Indels 29; Gaps 23;

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OY 715 DQPNVQC-IVALVI-I-FCSTITLCLVFPVKLITLITNDPATONRR 759
RESULT 8
ID MGR7_RAT STANDARD; PRT; 915 AA.
AC P35400;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.
GN GMR7 OR MGLUR7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC [1]
OC SEQUENCE FROM N.A.
OC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
OC MEDLINE: 94117433.
OC RA OKAMOTO N., HORI S., AKAZAWA C., HAYASHI Y., SHIGEMOTO R.,
OC MIZUO N., NAKANISHI S.;
OC "Molecular characterization of a new metabotropic glutamate receptor
OC mglur7 coupled to inhibitory cyclic AMP signal transduction.";
OC J. Biol. Chem. 269:1231-1236(1994).
OC [2]
OC SEQUENCE FROM N.A.
OC STRAIN-SPRAGUE-DAWLEY; TISSUE-OLFACTORY BULB;
OC MEDLINE: 94195260.
OC RA SAUGSTAD J.A., KINZIE J.M., MULVIHILL E.R., SEGGERSON T.P.,
OC WESTBROOK G.L.;
OC "Cloning and expression of a new member of the L-2-amino-4-
OC phosphonobutyric acid-sensitive class of metabotropic glutamate
OC receptors.";
OC Mol. Pharmacol. 45:367-372(1994).
OC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
OC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
OC ACTIVITY.
OC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
OC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED THROUGHOUT THE BRAIN.
OC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
OC STRONGEST, TO MGLUR4.
OC -----
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OC or send an email to license@isb-sib.ch).
OC CC
OC EMBL: D16817; BAA04092.1; -.
OC EMBL: U06832; AAA20655.1; -.
OC DR GCRDB: GCR_0945; -.
OC DR GCRDB: GCR_0946; -.
OC DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
OC DR PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
OC DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
OC DR PFAM: PF00003; 7tm_3; 1.
OC DR PFAM: PF01094; ANF_receptor; 1.
OC DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
OC Multi-gene family; Olfaction.
OC KW SIGNAL
OC FT CHAIN 1 32 POTENTIAL.
OC FT DOMAIN 33 915 METABOTROPIC GLUTAMATE RECEPTOR 7.
OC FT TRANSSEM 33 590 EXTRACELLULAR (POTENTIAL).
OC FT TRANSSEM 591 615 I (POTENTIAL).
OC FT TRANSSEM 616 627 CYTOPLASMIC (POTENTIAL).
OC FT TRANSSEM 628 648 II (POTENTIAL).
OC FT TRANSSEM 649 654 EXTRACELLULAR (POTENTIAL).
OC FT TRANSSEM 655 675 III (POTENTIAL).
OC FT TRANSSEM 676 702 CYTOPLASMIC (POTENTIAL).
OC FT TRANSSEM 703 723 IV (POTENTIAL).
OC FT TRANSSEM 724 753 EXTRACELLULAR (POTENTIAL).
OC FT TRANSSEM 754 775 V (POTENTIAL).
OC FT TRANSSEM 776 788 CYTOPLASMIC (POTENTIAL).

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FT	TRANSMEM	789	810	VI (POTENTIAL).
FT	DOMAIN	811	825	EXTRACELLULAR (POTENTIAL).
FT	TRANSME	826	850	VII (POTENTIAL).
FT	DOMAIN	851	915	CYTOPASMIC (POTENTIAL).
FT	CARBOHYD	98	98	POTENTIAL.
FT	CARBOHYD	458	458	POTENTIAL.
FT	CARBOHYD	486	486	POTENTIAL.
FT	CARBOHYD	572	572	POTENTIAL.
SQ	SEQUENCE	915 AA:	102231 MM:	AFAAD466 CRC32;
 Query Match 3.1%; Score 214; DB 1; length 915; Best Local Similarity 22.9%; Pred. No.1.03e-15; Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;				
Db	597 LAMGII-ATIFVMATEIRYNDPIVRASGRELSVYLGLTGFICY--IITF-L---MIA-	648		
OY	488 LTILIGIMSAFLFFN-IKNRNOGLIKHSSPMNNLIILIGMLSYASIFLFGIDGSFVE	546		
Db	649 KDVAVCSRRREFLGKMCISTALLTKNRRIREFEGOKSVYAPRLISPISQAITS	708		
OY	547 KEFEELCTVETWLTIVGYTTAFGAMFAKTWRVAHAIFFKNMK-K--KIIRDKLIVYG	603		
Db	709 LISVOLGVFI-WFGVDPPNIID-YD-EHKTMNPQA-RGVLK-CDIIDIQ-ICSL-G	761		
OY	604 MLTIID-CLICIQOAVDPRTVEKTSMEPPDPAGRDISIPLEHCENTHMHTIWIGIVA	662		
Db	762 YSILLMV-TC-TVVAIKRTGPENFNENAKPIGTWTTCIVMLAIPIFPGTAQSAEKLY	819		
OY	663 YKGLLMFCFPLAMEFRNVSIDA-LNDSKYIGMSYVNGVICMIGANAASFLLRPDPNVQ	721		
Db	820 IOTTTLTISMNASVALGMLYMPKVYIIIFPELVOKRKSF	863		
OY	722 C-IVALVI-I-FCSITTCLVEFPKILTLRTNDPDAATORRROF	762		
 RESULT 9 ID MGR7 HUMAN STANDARD: PRT: 915 AA. AC Q14831. DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 15-DEC-1999 (Rel. 39, Last annotation update) DE METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR. GN GRM7 OR MGUR7. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; OC Eutheria; Primates; Catarrhini; Homidae; Homo. RN [1] RP SEQUENCE FROM N.A. RC TISSUE-BRAIN: RX MEDLINE: 96437220. RX MAROFF A., PILILING C., HARRINGTON K., EMSON P.; RT "Human metabotropic glutamate receptor type 7: molecular cloning and mRNA distribution in the CNS"; RL Brain Res. Mol. Brain Res. 40:165-170(1996). RL [2] RP SEQUENCE FROM N.A. RX MEDLINE: 98141892. RX WU S., WRIGHT R.A., ROCKEY P.K., BURETT S.G., ARNOLD J.S., RA ROSTECK P.R. JR., JOHNSON B.G., SCHORPP D.D., BELAGAJE R.M.; RT "Group III human metabotropic glutamate receptors 4, 7 and 8: molecular cloning, functional expression, and comparison of pharmacological properties in RGT cells"; RT Brain Res. Mol. Brain Res. 53:88-97(1998). RT -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY. CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS. CC STRONGEST, TO MOLDR4. ----- CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its				

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CC		or send an email to license@isb-sib.ch .
DR	EMBL: X94552; CAA64245.1;	-
DR	EMBL: U92458; AAB51763.1;	-
DR	MIM: 604101;	-
DR	GCRDB; GCR_1890;	-
DR	GCRDB; GCR_2071;	-
DR	PROSITE; PS00979; G_PROTEIN_RECPEP_F3_1;	1.
DR	PROSITE; PS00980; G_PROTEIN_RECPEP_F3_2;	1.
DR	PROSITE; PS00981; G_PROTEIN_RECPEP_F3_3;	1.
DR	PFAM; PF00003; 7tm_3;	1.
KW	PFAM; PF01094; ANF_receptor;	1.
KM	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;	
FT	Multigene family; olfaction; Polymorphism.	
FT	SIGNAL	1 32
FT	CHAIN	33 915
FT	DOMAIN	33 590
FT	TRANSMEM	591 615
FT	DOMAIN	616 627
FT	TRANSMEM	628 648
FT	DOMAIN	649 654
FT	TRANSMEM	655 675
FT	DOMAIN	676 702
FT	TRANSMEM	703 723
FT	DOMAIN	724 753
FT	TRANSMEM	754 775
FT	DOMAIN	776 788
FT	TRANSMEM	789 810
FT	DOMAIN	811 825
FT	TRANSMEM	826 850
FT	DOMAIN	851 915
FT	CARBOHYD	98 98
FT	CARBOHYD	458 458
FT	CARBOHYD	486 486
FT	CARBOHYD	572 572
FT	VARIANT	433 433
SEQ	SEQUENCE	915 AA; 102250 MW; 1B278E39 CRC32; /Frtid=VAR_003584.
Query Match	Best Local Similarity	3.1%; Score 214; DB 1; Length 915;
Matches	65; Conservative	87; Mismatches 106; Indels 26; Gaps 22;
Db	597 LAMILII-ATIFVMAVFPIRYNDPTPIVASGDELAVLLTGFIQL--ITTF-L---MIA-	648
Oy	488 LTIIIDIMASAFLEPPN-IKNRQKIKTKSSPYNNMLLIIGSLSYASTIFLEGIDGSFVSE	546
Db	649 KPDVAVCFSRRVFLGLGMCISYAALLTNTKRIYRFEGGGKSVPAPRLISPSTOLATSS	708
Oy	547 KTFELLCIVRWILLVGTTAFGAMFAKTMYVHAIFKRVAKK-K--KIIDQILLVIYG	603
Db	709 LISVOLCLVFI-WGVDPENIITD-YD-EHKTMNPEDA-RGVLK-CDTLDQT-ICSL-G	761
Oy	604 MLTIIDL-CILICMOAVDLRTVEYSMEBDPADGISIRPLEHCENTHMTIWGIIVA	662
Db	762 YSILIIM-TC-TVAIAIKRGVPEPNNEKPIGLFMITYTCIYMALFIPIFGSTAQSARKLY	819
Oy	663 YKGLMIAGCPLAWETRNVSIPA-LNSCKTIGMSVMYNGVICIIIGAASFELTRDPNVQF	721
Db	820 IQTTLTITISMNLASVALGMLYMPKVYIIIPHELINTOKRKRSF	863
Oy	722 C-YVALVI-I-FCSGITTLCLVFPVKRLTLKRTPDAQAONRRQF	762
RESULT	ID	10
AC	MGR5_RAT	STANDARD; PRT; 1203 AA.
DT	P31424;	
DT	01-JUL-1993 (Rel. 26, Created)	
DT	01-NOV-1995 (Rel. 32, Last sequence update)	
DT	15-DEC-1999 (Rel. 39, Last annotation update)	

FT	DOMAIN	827	1203	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	88	88	POTENTIAL.
FT	CARBOHYD	209	209	POTENTIAL.
FT	CARBOHYD	377	377	POTENTIAL.
FT	CARBOHYD	381	381	POTENTIAL.
FT	CARBOHYD	444	444	POTENTIAL.
FT	CARBOHYD	733	733	POTENTIAL.
FT	VARSPIC	876	907	MISSING (IN ISOFORM 5A).
SO	SEQUENCE	1203 AA;	131885 MW; 2955EA33 CRC32;	
Query Match 3.1%; Score 215; DB 1; Length 1203;				
Best Local Similarity 28.3%; Pred. No. 6,98e-16;				
Matches 54; Conservative 57; Mismatches 61; Indels 19; Gaps 1				
D	655	AMSYALVTYKTNRIARILAGSK-KKICTKKPRMSACA-OLVIAF-ILIC--IQ-LGIT 707		
Q	565	TTAFGAFATKTVHVAHIFKVKMKKKIKIDOKLIVVGMLIDLCILICIMQADVPLRRT 624		
D	708	VALFIMPEPDMHDYSIREVYLICNTMNGV-VNPL-GYGNLLIL-SCTFAYFRTNVP 764		
Q	625	VERKSEMPDAGRI-SIRPLEHCHECINTHTLGLVAYAKGLMLFGC-FLAMETRNVS 682		
D	765	-ANFNEAKYIAFTMYTTCIIMLAFAVPI-YFGSNYKLIITMCF-S-VSL-SATVALGCM-FV 818		
Q	683	IPALNDSKVIIGMSYVNGIMCIIGAASFILTRDQPNWQCIYALVIFPCSTITL-CLVEFV 741		
D	819	PKYIILAKPE 829		
Q	742	PKLITLRTNPD 752		
RESULT 11				
ID	MG95_HUMAN	STANDARD;	PRT;	1212 AA.
AC	P41594;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-OCT-1996 (Rel. 34, last sequence update)			
DT	15-DEC-1999 (Rel. 39, last annotation update)			
DE	METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.			
GN	GMR5 OR MGUR5.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homiidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN.			
RX	MEDLINE; 94197696.			
RA	MINAKAMI R., KATSUKI F., YAMAMOTO T., NAKAMURA K., SUGIYAMA H.;			
RT	"Molecular cloning and the functional expression of two isoforms of			
RT	human metabotropic glutamate receptor subtype 5.";			
RL	Biochem. Biophys. Res. Commun. 199;1136-1143(1994).			
RN	[2]			
RP	REVISIONS.			
RA	KATSUKI F.;			
RL	submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE OF 860-952 FROM N.A.			
RC	TISSUE-BRAIN;			
RX	MEDLINE; 93343913.			
RA	MINAKAMI R., KATSUKI F., SUGIYAMA H.;			
RT	"A variant of metabotropic glutamate receptor subtype 5: an			
RT	evolutionally conserved insertion with no termination codon.";			
RL	Biochem. Biophys. Res. Commun. 194;622-627(1993).			
CC	1- FUNCTION. RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS			
CC	IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-			
CC	MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-			
CC	CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED			
CC	CHLORIDE CURRENT.			
CC	1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	1- ALTERNATIVE PRODUCTS: TWO ISOFORMS; 5A (SHOWN HERE) AND 5B; ARE			
CC	PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF			
CC	32 RESIDUES.			
CC	1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.			
CC	STRONGEST, TO MGUR1.			

DR EMBL: X12874; CAA31367.1; .
 DR PIR: S05480; OYURGA.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PFAM: PF00069; PKinase; 2.
 DR PFAM: PF01094; ANF_receptor; 1.
 DR Receptor; Transmembrane; Glycoprotein; Phosphorylation; Lyase;
 KW GMP synthesis; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 986
 FT DOMAIN 22 507
 FT TRANSMEM 508 528
 FT DOMAIN 529 986
 FT DOMAIN 568 836
 FT CARBOHYD 185 185
 FT CARBOHYD 361 361
 FT CARBOHYD 410 410
 FT SEQUENCE 986 AA; 11284 MW; 68BFC466 CRC32;
 Query Match 2.88; Score 195; DB 1; Length 986;
 Best Local Similarity 26.08; Pred. No. 1,36e-12;
 Matches 52; Conservative 49; Mismatches 91; Indels 8; Gaps 7;
 DB 2 ATTLLELLVVAIVTWRSAITLHPYINIDRGKPKLHGMTSWTNADNSGCTGPPS 61
 19 PPARLLLLPLPLPLPLPGA-WGMAGAPRPPSSPPLSLGMLPLKREYAKSGISGRV 77
 DB 62 AGAPPLAIOYANNDMDILHGVDINFEWVDTHCDINLGMALSDMKRG--FLGYIGPGCG 119
 78 LPAVELALIEQIRNE-SLIRYFLDLRYDTECDNAKGLKAFYDAIKYGNHLMVFGVCIP 136
 DB 120 CTYGRRLASALN-FPMIDYA-CDENPV-SNKEFYPTLRTIPRSQYVDSLLTLMDYDM 176
 137 SV-TSILAESQGMNLVQSLAFTPYLADKKKPYFETPSDVAAPALIKLKHQW 195
 DB 177 NQTVVVENITKRYRNPNTM 196
 OY 196 KRVGTLTDVQRESEVRNDL 215
 RESULT 15
 ID MGR2_RAT STANDARD; PRT; 872 AA.
 AC P31421;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR.
 GN GRM2 OR MGLUR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE: 92110002.
 RA TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;
 RT "A family of metabotropic glutamate receptors.";
 RL Neuron 8:169-179(1992).
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
 CC MAY MEDATE SUPPRESSION OF NEUROTRANSMISSION OR MAY BE INVOLVED IN
 CC SYNAPTOGENESIS OR SYNAPTIC STABILIZATION.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS AND PROMINENT
 CC EXPRESSION IS SEEN IN GOLGI CELLS OF THE CEREBELLUM AND SOME
 CC PARTICULAR NEURONAL CELLS IN OTHER BRAIN REGIONS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST, TO MGLUR3.
 CC -----
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 CC -----
 DR EMBL: M92075; -. NOT_ANNOTATED_CDS.
 DR PIR: JH0561; JH0561.
 DR HSSP: P06612; IECU.
 DR GCRDB: GCR0361; .
 DR PROSITE: PS00979; G_PROTEIN_RECEPT_F3_1; 1.
 DR PROSITE: PS00980; G_PROTEIN_RECEPT_F3_2; 1.
 DR PROSITE: PS00981; G_PROTEIN_RECEPT_F3_3; 1.
 DR PFAM: PF01094; ANF_receptor; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Multigene family.
 FT SIGNAL 1 18
 FT CHAIN 19 872
 FT DOMAIN 19 567
 FT TRANSMEM 568 590
 FT DOMAIN 591 604
 FT TRANSMEM 605 625
 FT DOMAIN 626 636
 FT TRANSMEM 637 655
 FT DOMAIN 656 679
 FT TRANSMEM 680 700
 FT DOMAIN 701 725
 FT TRANSMEM 726 747
 FT DOMAIN 748 760
 FT TRANSMEM 761 783
 FT DOMAIN 784 793
 FT TRANSMEM 794 819
 FT DOMAIN 820 872
 FT CARBOHYD 203 203
 FT CARBOHYD 286 286
 FT CARBOHYD 338 338
 FT CARBOHYD 402 402
 FT CARBOHYD 547 547
 FT SEQUENCE 872 AA; 95773 MW; C3C3467E CRC32;
 Query Match 2.78; Score 189; DB 1; Length 872;
 Best Local Similarity 24.78; Pred. No. 1,25e-11;
 Matches 55; Conservative 66; Mismatches 80; Indels 22; Gaps 19;
 DB 611 GGVFLCYCMTEFFFLA-KPSTAVCTLRRLGIGTAFSCYSALLTKTNRIARFGAREGAQ 669
 532 ASIFL-FELDSSEFVSEKTEFTLCTVETWILTVGYTAFGAMPAKRWHAIFKRVK--MK 588
 DB 670 RPRFSPASOYALICLALISGOLLIVAMLVPE-PGT-GK-ETAPER--REV-V-TL--R 720
 589 K-KIIOKQLVIVYGMLLDLCILICMOAVDPRLRTYKYSMEFDPAGRIDISIRPLEH 647
 DB 721 CNHRDASK-LGSL-AYNVLLIAL-CTLYAFKTRKCP-ENFNEAKFIFTMYTTCIIMLAF 776
 648 CENTHMTWLGIVAYKGLMLFGCFL-AMETRNVSIPALNSKRYIGMSYVNVGIMCIG 706
 DB 777 LPPIFYTSDDYRQVOTTCMCVSLSGVYGLCP-PAPKRIHIL 818
 707 AAVSFLTDQPNVQPCIALVILIFCSTITL-CLVFPKIL-TIL 747

Search completed: Wed Apr 19 21:55:23 2000
 Job time : 219 secs.

QY	74	GRVLPAVELAIEQIRNE-SILRPUFLDLRLYDTECDNAGKLAFYDAIKYGNHNLAVFG	1322
Db	244	G-CSSVTLVAEAAARMNLLVLSYSSSPALSNQRPTFRPHPSATLHNPRLVLFK	302
QY	133	GVCSVSVSIASESLOGNLLVOLSAAVTPVLADKKRYFFRRVPSDANPAILKLKH	1922
Db	303	MGMKKITTIOQTTEVFSTDLDEERKEAGIEITTFQSFSDPAVYVNMILKODAAIIV	3622
QY	193	YOMKRVGTLIDVOFRFSEVRNDLTGVLGEDIETSDIESNDPCTSVYKLLKGNDAIIL	2522
Db	363	GLFYETEARKEVCEYKERLEFGKKYVFLIGVYADNMF-KIY-DP-SINCTVDEMTAVE	4192
QY	253	GOFOJNMAAKVFCATSEBNMYGSKYOWITIPQWYPPSMWEOYHTPANSRCLRKLLAAE	3122
Db	420	GHTTEIYVLMNPANTRISIMNTSOEYFEKLTRLKRPETGGQZAPLAYDIMALALA	4192
QY	313	GYIVDEPPLSKOIKITISGTRPOOY-EREYN-KRSGVGSKPH-G-VAYDGLWYIAKT	3682
Db	480	LNTKSGG--GGRSQVRLDEDFYNNQTLTDQYRAMNSSPFGVGHVFPASGSRMWTL	5372
QY	369	LORMETLHASRHOIRIODENYDHTLIGRIILNANMETNFGVGYOYVF-RNGBRKTIK	4272
Db	538	IEOPGGSYKRIGYDYSTKDDLSW-SKTDKWIGSPSPADQTLVIKTRPLFSOKLFISVY	5362
QY	428	FTQRODSSEVYGEYVNAVDTLEIINTIRGSEPPKDKTILIEQLRKISLPIYSTLSA	4872
Db	597	LSLSGIVLAVVCLSPNIYNSHVRYIONSQPNLNNLTVAGCSLAAVFPGLDGYHIGRN	6562
QY	488	LTIIGMIAVSAPLEFNKIKNRNOKILIKSSPMMNLILGGMLSVASIFELGLDGSFVSEK	5472
Db	657	QEPFYCAQRMLLGLGFSLGYSGMETIKWYHGFETKKEKKEMKRLPEPMKIYATVGL	7162
QY	548	TFETLCYVTRWILVGTITAGAFATWRHALF--KNYAK-KKILIKODKLVIYVGM	6042
Db	717	VGMVULTAIMOYDPLHRTLETPAKKEPKEDIVSILPOLHCSSRKMTWLGIFYGK	7762
QY	605	LLIDLCILICQWADPLRLRYTEKSMEDDPAGRIDISIRPLEHCEHNHMTIMGIYAYK	6662
Db	777	GLLLLLGFLAVLEFKSVSTEKINDHRAVGMAIIVAAVCLITAPYVMTLSSQODAAFA	8362
QY	665	GLMLMFGCEFLAMETRNVSIPALNDSKYIGMSVYVNGCIIGAASFLTRDOPWQCIY	7242
Db	837	SLATYESSYITLVLEVFKMRILTRGE	8642
QY	725	ALVITPFCSTITLCAVDPKLTITKINPD	7522

RESULT	2	
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TITLE	149142	#type complete
ORGANISM		metabotropic glutamate receptor 8 - mouse
DATE	02-Jul-1996	#formal_name Mus musculus #common_name house mouse
	13-Sep-1998	#sequence_revision 02-Jul-1996 #text_change
ACCESSIONS	149142	
REFERENCE	149142	
#authors	Duvolsin, R.M.; Zhang, C.; Ramonell, K.	
#journal	J. Neurosci. (1995) 15:3075-3083	
#title	A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb.	
#cross-references	MUID:95239344	
#accession	I49142	
#status	preliminary; translated from GB/EMBL/DBJ	
#molecule_type	mRNA	
#residues	1-908	#label RES
#cross-references	EMBL:U17252; NID:g854728; PID:g854729	
GENETICS		
#gene	mGluR8	
CLASSIFICATION		
KEYWORDS	#superfamily metabotropic glutamate receptor 4	
SUMMARY	#neurotransmitter receptor	
	#length 908 #molecular_weight 101413 #checksum 2996	
Query Match	3.5%;	Score 241; DB 2; Length 908;

Best Local similarity 22.1%; Pred. No. 7,82e-17;
Matches 64; Conservative 99; Mismatches 101; Indels 25; Gaps 22;

	RESULT	3	A46742	#type complete
	ENTRY			metabotropic glutamate receptor, mGluR6 - rat
	TITLE			#formal_name Rattus norvegicus #common_name Norway rat
	ORGANISM			21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
	DATE			29-Jan-1999
	ACCESSIONS		A46742	
	REFERENCE		A46742	
	#authors		Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto,	
	#journal		R.; Mizuno, N.; Nakanishi, S.	
	#title		J. Biol. Chem. (1993) 268:11868-11873	
			Molecular characterization of a novel retinal metabotropic	
			molecular receptor mGluR6 with a high agonist selectivity	
			for L-2-amino-4-phosphonobutyrate.	
	#cross-references		MUID:93280152	
	#accession		A46742	
	#status		preliminary	
	#molecule_type		nucleic acid	
	#residues		1-871 ##label NAK	
	#cross-references		GB:D13963; NID:g391856; PID:t1003572; PID:g391857	
	##experimental_source		retina	
	#note		sequence extracted from NCBI backbone (NCBIN:133246,	
			NCBIP:133250)	
	CLASSIFICATION		#superfamily metabotropic glutamate receptor 4	
	KEYWORDS		G protein-coupled receptor; transmembrane protein	
	SUMMARY		#length 871 #molecular_weight 95088 #checksum 3942	
	Query Match		3.4%; Score 236; DB 2; Length 871;	
	Best Local Similarity		22.9%; Pred. No. 4,22e-16;	
	Matches		64; Conservative 90; Mismatches 102; Indels 24; Gaps 21	
Df	586	LAVIG-IMATTTTATFERNHDFPIVASGSELVLTGLFIYA-I-TP-L--WVAE	638	
Oy	488	ITIIQIMASALEPFINNRNOK-VIKSSPYNNLLILGMLSTAYSLFELGDSYSE	546	
Df	639	PC-AAICAAARLLDCLGTLSALTLTKNTIYRFEGGKRSVPPIPTPSOLVTIFG	697	
Oy	547	KTFELLCIVRTMILVGTTTAAGAMFAFTWVHAIFKNVK--MKKK-IIRQKLVIYG	603	
Df	698	ITSLOVGVIAWLGAOPHSVID-YE-EORTVDPEQA-RGYLK-CDSMSDL-TGCL-GY	751	
Oy	604	MLIIDLCLILICQANDPLRRVEKYSMBPDAGRDISIRPLEHCENTHMIIWGIYAY	663	
Df	752	-SLLMATVC-IYYAIIKAAGVETFEAKRPFGFTMTTCIIMLAVPPIFFGTAOSAERTI	809	
Oy	664	KSLIMLFGEFLAMETRNNSPI-ALNDSKYIGMSYVNGIMCIIIGAASFTRDPNPVQC	722	
Df	810	QTTLTVSLTSASVSLGMIVPKRYVILLPHDEQVOKRK	849	

QY 723 -IVALVI-I-FCSTITLCLVEPKLITLRTNPDATQNR 759

RESULT 4

ENTRY JH0563 #type complete

TITLE metabotropic glutamate receptor 4 precursor - rat

ORGANISM #formal_name Rattus norvegicus #common_name Norway rat

DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998

ACCESSIONS JH0563

REFERENCE JH0561

#authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.

#journal Neuron (1992) 8:169-179

#title A family of metabotropic glutamate receptors.

#cross-references MUID:92110002

#accession JH0563

#molecule_type mRNA

#residues 1-912 #label TAN

COMMENT #experimental_source brain

This protein is coupled to a G protein and evokes a variety of functions by mediating intracellular signal transduction.

CLASSIFICATION #superfamily metabotropic glutamate receptor 4

KEYWORDS G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

FEATURE

1-32

33-912

#domain signal sequence #status predicted #label SIG\

#product metabotropic glutamate receptor 4 #status predicted #label MET\

588-610

625-645

657-675

700-720

751-772

786-807

822-847

98,301,454,484,

569

#binding-site carbohydrate (Asn) (covalent) #status predicted\

621,689,695,859,

870

#binding-site phosphate (Ser) (covalent) #status predicted

SUMMARY #length 912 #molecular-weight 101818 #checksum 808

Query Match 3.3%; Score 225; DB 2; Length 912;

Best Local Similarity 22.6%; Pred. No. 1,66e-14;

Matches 65; Conservative 93; Mismatches 101; Indels 29; Gaps 23;

Db 588 AVLPFLAVVG-IAATLFVVVTVRYNDPIVAKSGRELSYVLACIFLCYATPFL--M- 643

QY 483 SILSA-LTIIGMIMASAFLEFN-IKNRNOKLIKMSPPYNNLLIIGMLSYASIFLEGLD 540

Db 644 ---IAEPDLGT-CSLRIFLGLCMSISYALLTKTRIRYIFEQGRSVSAPRFISPASQ 699

QY 541 GSFSVSEKTFEFLCTYRWILTVGTTAFGAMFAKTRVHAIFRNVK--MKK-KIKDKQL 597

Db 700 LAIT--FILISLQGLGICVFWVDPSSHVD--FQDQRTIDPR-FA-RGVK-CDISDLSL 753

QY 598 LVIYVGMILLDLCL-IC-WQAVDPLRRTYEKSMEDPDAGROISIRPLEHCENHMTI 655

Db 754 -ICLL-GYSMLMV-TC-TVYAIKTRGVPEFNEARPIGFTWYTCIWLAFPIPFQTS 809

QY 656 WLGIYVAYKGLMLFCGFLAMETRNVSIP-ALNDSKYIGMSYVNVGIMCIGAAVSFLR 714

Db 810 QSADKLYIQTTTLTVSVLSASYSGLMLYMPKYIILFHPDQNVPRK 857

QY 715 DQPNVQFC-IVALVI-I-FCSTITLCLVEPKLITLRTNPDATQNR 759

RESULT 5

ENTRY I58149 #type complete

TITLE metabotropic glutamate receptor - rat

ORGANISM #formal_name Rattus norvegicus #common_name Norway rat

DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change

ACCESSIONS 13-Sep-1998

REFERENCE I58149

#authors O'Hara, P.J.; Sheppard, P.O.; Thøgersen, H.; Venezia, D.; Haldeman, B.A.; McGrane, V.; Houamed, K.M.; Thomsen, C.; Gilbert, T.L.; Mulvihill, E.R.

#journal Neuron (1993) 11:41-52

#title The ligand-binding domain in metabotropic glutamate receptors is related to bacterial periplasmic binding proteins.

#cross-references MUID:93332699

#accession I58149

#status Preliminary; translated from GB/EMBL/DBJ

#molecule_type mRNA

#residues 1-912 #label RES

GENETICS #cross-references GB:M90518; NID:g205400; PID:g205401

CLASSIFICATION #superfamily metabotropic glutamate receptor 4

KEYWORDS neurotransmitter receptor

SUMMARY #length 912 #molecular-weight 101846 #checksum 818

Query Match 3.3%; Score 225; DB 2; Length 912;

Best Local Similarity 22.6%; Pred. No. 1,66e-14;

Matches 65; Conservative 93; Mismatches 101; Indels 29; Gaps 23;

Db 588 AVLPFLAVVG-IAATLFVVVTVRYNDPIVAKSGRELSYVLACIFLCYATPFL--M- 643

QY 483 SILSA-LTIIGMIMASAFLEFN-IKNRNOKLIKMSPPYNNLLIIGMLSYASIFLEGLD 540

Db 644 ---IAEPDLGT-CSLRIFLGLCMSISYALLTKTRIRYIFEQGRSVSAPRFISPASQ 699

QY 541 GSFSVSEKTFEFLCTYRWILTVGTTAFGAMFAKTRVHAIFRNVK--MKK-KIKDKQL 597

Db 700 LAIT--FILISLQGLGICVFWVDPSSHVD--FQDQRTIDPR-FA-RGVK-CDISDLSL 753

QY 598 LVIYVGMILLDLCL-IC-WQAVDPLRRTYEKSMEDPDAGROISIRPLEHCENHMTI 655

Db 754 -ICLL-GYSMLMV-TC-TVYAIKTRGVPEFNEARPIGFTWYTCIWLAFPIPFQTS 809

QY 656 WLGIYVAYKGLMLFCGFLAMETRNVSIP-ALNDSKYIGMSYVNVGIMCIGAAVSFLR 714

Db 810 QSADKLYIQTTTLTVSVLSASYSGLMLYMPKYIILFHPDQNVPRK 857

QY 715 DQPNVQFC-IVALVI-I-FCSTITLCLVEPKLITLRTNPDATQNR 759

RESULT 6

ENTRY A49874 #type complete

TITLE metabotropic glutamate receptor 7 - rat

ALTERNATE_NAMES metabotropic glutamate receptor mGluR7

ORGANISM #formal_name Rattus norvegicus #common_name Norway rat

DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Sep-1998

ACCESSIONS A49874; I57954

REFERENCE A49874

#authors Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.

#journal J. Biol. Chem. (1994) 269:1231-1236

#title Molecular characterization of a new metabotropic glutamate receptor mGluR7 couple to inhibitory cyclic AMP signal transduction.

#cross-references MUID:94117433

#accession A49874

#status Preliminary; translated from GB/EMBL/DBJ

#molecule_type mRNA

#residues 1-915 #label RES

GENETICS #cross-references GB:D16817; NID:g458728; PID:g458729

REFERENCE I57954

#authors Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L.

#journal Mol. Pharmacol. (1994) 45:367-372

#title Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid-sensitive class of

	#cross-references	MIMD:94135260	metabotropic glutamate receptors
	#accession	I57954	
	##status	preliminary; translated from GB/EMBL/DDBJ	
	##molecule_type	mRNA	
	##residues	1-915 ##label RE2	
	##cross-references	EMBL:006832; NID:g459657; PID:g459658	
	GENETICS		
	#gene	MGUR7	
	CLASSIFICATION	#superfamily metabotropic glutamate receptor 4	
	KEYWORDS	neurotransmitter receptor	
	SUMMARY	#length 915 #molecular-weight 102231 #checksum 1873	
	Query Match	3.1%; Score 214; DB 2; Length 915;	
	Best Local Similarity	22.9%; Pred. No. 6,22e-13;	
	Matches	65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;	
Db	597 LAMGII-ATTFVMTFIRYNDPIRVDIYASRGHLSYLLTGIFLCY--ITTF-L---MIA-648		
Oy	488 LTILGMIVASAFLEFFN-IKNNOQLIKMSPPYNNLIIILIGMLSYASIFLFGDGFSVE 546		
Db	649 KPDVAQCFERVFVLGLGCISYALTLKTNKTVIFEFQGGKSVAAPLISPQLATSS 708		
Oy	547 KPEFLTCVRKWILLVGTTTAFGAMPKTRVHAIFNKVK-K-KIIDOKLIIVYG 603		
Db	709 LISVOLLGEVI-WGVDPENIIID-YD-EHKTMPEQA-RGVAK-CDITDLQI-TCSL-G 761		
Oy	604 MLTIIDL-CILICWOAVDPLRTVERKYSMEPDPAGRDISIPLLEHCENTHTIWLGIYA 662		
Db	762 YSILMV-TC--TYAAIKRGVDEPNNEAKPIGFMYTTCIVWLAFLPIFPGTAGSAEKLY 819		
Oy	663 YKGLMLGCGELAWETRNVSIIPA-LNDSKIIGMSVINVGMCITIGAASFLTRDPNQVF 721		
Db	820 IQTTLTISNMLSASVALGMLMPRYEIIIPHEINVOQRKRP 863		
Oy	722 C-IVALVI-I-FCSTITLCIVFVPRLTLTRNPDAQNRRPFQF 762		
RESULT	7		
ENTRY	A42916	#type complete	
TITLE		metabotropic glutamate receptor mglur5 - rat	
ORGANISM		formal name Rattus norvegicus #common_name Norway rat	
DATE		04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 29-Jan-1999	
ACCESSIONS	A42916		
REFERENCE	A42916		
#authors	Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakamishi, S.		
#journal	J. Biol. Chem. (1992) 267:13361-13368		
#title	Molecular characterization of a novel metabotropic glutamate receptor mglur5 coupled to inositol phosphate/Ca2+ signal transduction.		
#cross-references	MIMD:92317054		
#accession	A42916		
##status	Preliminary		
##molecule_type	mRNA		
##residues	1-1171 ##label ABE		
##cross-references	GB:d10891; NID:g220813; PID:d1002186; PID:g220814		
##experimental_source	Brain		
##note	sequence extracted from NCBI backbone (NCBIN:107749, NCBI:P107750)		
KEYWORDS	G protein-coupled receptor; transmembrane protein		
SUMMARY	#length 1171 #molecular-weight 128289 #checksum 8594		
Query Match	3.1%; Score 215; DB 2; Length 1171;		
Best Local Similarity	28.3%; Pred. No. 4,49e-13;		
Matches	54; Conservative 57; Mismatches 61; Indels 19; Gaps 17		
Db	655 AMSYSLATKTNRIAIITLGSK-KKICTCTKKPFNSACA-QLVIAF-LITC--IQ-LGII 707		
Oy	565 TYAEGMAPKTRVHAIFNKVKKKKLIKDKQLIVYGSMILIDICILICQWADPLART 624		
Db	708 VALFIIEPDIIMHDPSIREVYLICNTTNUG-VTP-L-GYNGLLIL-SCTFYAKTRNVP 764		

OY	625	VEKSMEDPDAGRII-SIRPLEHCENTHTMTIMLGIVAAKGLMLFGC-FLAWETRNRVS	682
Db	765	-ANENAKRYIAFTYTCIILMAFVPI-YFGSNKYITTCF-S-VSL-SATVALGCM-FV	818
OY	683	IPALNDSKYSIGMSYNYNGIMCIIIGAAVSFLTRDPQNVQFCIVALYIIFCSTITL-CLAFV	741
Db	819	PKYVYIIIAKPE	829
OY	742	PKLITLRTPD	752
RESULT	8		
ENTRY	JC2132	#type complete	
TITLE	metabotropic glutamate receptor 5 A - human		
ORGANISM	#formal_name Homo sapiens #common_name man		
DATE	28-Aug-1995 #sequence_revision 07-Oct-1994	#text_change	
ACCESSIONS	JC2132		
REFERENCE	JC2131		
#authors	Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.		
#journal	Biochem. Biophys. Res. Commun. (1994) 199:1136-1143		
#title	Molecular cloning and the functional expression of two isoforms of human metabotropic glutamate receptor subtype 5.		
#cross_references	MUID:94197696		
#accession	JC2132		
##molecule_type	mRNA		
##residues	1-1180 ##label MIN		
COMMENT	This protein is coupled to guanine nucleotide binding proteins.		
KEYWORDS	glycoprotein; neurotransmitter; receptor; Transmembrane protein		
FEATURE			
580-604	##domain transmembrane #status predicted #label TM1\		
617-637	##domain transmembrane #status predicted #label TM2\		
644-664	##domain transmembrane #status predicted #label TM3\		
694-714	##domain transmembrane #status predicted #label TM4\		
738-759	##domain transmembrane #status predicted #label TM5\		
773-794	##domain transmembrane #status predicted #label TM6\		
803-827	##domain transmembrane #status predicted #label TM7		
SUMMARY	#length 1180 #molecular_weight 129053 #checksum 237		
Query Match	3.1%; Score 215; DB 2; Length 1180;		
Best Local Similarity	28.3%; Pred. No. 4,496-13;		
Matches	54; Conservative 57; Mismatches 61; Indels 19; Gaps 17.		
Db	656	AMYSALVTKTRIRIAIRIGASK-KKICTKKRPFSACA-QLVIAF-LIIC---IO-LGI	708
OY	565	TAFGMAEPKATRYVAIRFAIKRYKMKKKIKDKDLIVYGMILLDLCLICQAVDPLRRT	624
Db	709	VALFMEPPDINHDPISIREVYLICNTNLGV-VTP-L-GYNGLLIL-SCITYAETKTRNP	765
OY	625	VEKYSMEPPDAPRDI-SIRPLEHCENTHTMTIMLGIVAAVGLMLTFCG-FLAWETRNV	682
Db	766	-ANENAKRYIAFTYTCIILMAFVPI-YFGSNKYITTCF-S-VSL-SATVALGCM-FV	819
OY	683	IPALNDSKYSIGMSYNYNGIMCIIIGAAVSFLTRDPQNVQFCIVALYIIFCSTITL-CLAFV	741
Db	820	PKYVYIIIAKPE	830
OY	742	PKLITLRTPD	752
RESULT	9		
ENTRY	JC2131	#type complete	
TITLE	metabotropic glutamate receptor 5 B - human		
ORGANISM	#formal_name Homo sapiens #common_name man		
DATE	28-Aug-1985 #sequence_revision 07-Oct-1994	#text_change	
ACCESSIONS	JC2131		
REFERENCE	JC2131		
#authors	Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.;		

OY	625	VEKSMEDPDAGRII-SIRPLEHCENTHTMTIMLGIVAAKGLMLFGC-FLAWETRNRVS	682
Db	765	-ANENAKRYIAFTYTCIILMAFVPI-YFGSNKYITTCF-S-VSL-SATVALGCM-FV	818
OY	683	IPALNDSKYSIGMSYNYNGIMCIIIGAAVSFLTRDPQNVQFCIVALYIIFCSTITL-CLAFV	741
Db	819	PKYVYIIIAKPE	829
OY	742	PKLITLRTPD	752
RESULT	8		
ENTRY	JC2132	#type complete	
TITLE	metabotropic glutamate receptor 5 A - human		
ORGANISM	#formal_name Homo sapiens #common_name man		
DATE	28-Aug-1995 #sequence_revision 07-Oct-1994	#text_change	
ACCESSIONS	JC2132		
REFERENCE	JC2131		
#authors	Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.		
#journal	Biochem. Biophys. Res. Commun. (1994) 199:1136-1143		
#title	Molecular cloning and the functional expression of two isoforms of human metabotropic glutamate receptor subtype 5.		
#cross_references	MUID:94197696		
#accession	JC2132		
##molecule_type	mRNA		
##residues	1-1180 ##label MIN		
COMMENT	This protein is coupled to guanine nucleotide binding proteins.		
KEYWORDS	glycoprotein; neurotransmitter; receptor; transmembrane protein		
FEATURE			
580-604	##domain transmembrane #status predicted #label TM1\		
617-637	##domain transmembrane #status predicted #label TM2\		
644-664	##domain transmembrane #status predicted #label TM3\		
694-714	##domain transmembrane #status predicted #label TM4\		
738-759	##domain transmembrane #status predicted #label TM5\		
773-794	##domain transmembrane #status predicted #label TM6\		
803-827	##domain transmembrane #status predicted #label TM7		
SUMMARY	#length 1180 #molecular_weight 129053 #checksum 237		
Query Match	3.1%; Score 215; DB 2; Length 1180;		
Best Local Similarity	28.3%; Pred. No. 4,496-13;		
Matches	54; Conservative 57; Mismatches 61; Indels 19; Gaps 17.		
Db	656	AMYSALVTKTRIRIAIRIGASK-KKICTKKRPFSACA-OLVIAF-LIIC---IO-LGI	708
OY	565	TAFGMAEPKATRYVAIRFAIKRYKMKKKIKDKDLVLVYGMLLDLCILQGVADPLRRT	624
Db	709	VALFMEPPDINHDPISIREYVLLICNTNLGV-VTP-L-GYNGLLIL-SCITYAETKTRNP	765
OY	625	VEKYSMEPPDAPRDI-SIRPLEHCENTHTMTIMLGIVAYAGLLMLFGC-FLAWETRNV	682
Db	766	-ANENAKRYIAFTYTCIILMAFVPI-YFGSNKYITTCF-S-VSL-SATVALGCM-FV	819
OY	683	IPALNDSKYSIGMSYNYNGIMCIIIGAAVSFLTRDPQNVQFCIVALYIIFCSTITL-CLAFV	741
Db	820	PKYVYIIIAKPE	830
OY	742	PKLITLRTPD	752
RESULT	9		
ENTRY	JC2131	#type complete	
TITLE	metabotropic glutamate receptor 5 B - human		
ORGANISM	#formal_name Homo sapiens #common_name man		
DATE	28-Aug-1985 #sequence_revision 07-Oct-1994	#text_change	
ACCESSIONS	JC2131		
REFERENCE	JC2131		
#authors	Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.;		

Db 177 NOVVENITKRYNVENTM 196
 OY 196 KRVGTITODVORSEVRNDL 215

RESULT 12
 ENTRY JH0561 #type complete
 TITLE metabotropic glutamate receptor 2 precursor - rat
 ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
 DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998

ACCESSIONS JH0561
 REFERENCE JH0561
 #authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
 #journal Neuron (1992) 8:169-179
 #title A family of metabotropic glutamate receptors.
 #cross-references MUID:92110002

FEATURE 1-872 #label TAN
 #residues 1-872 #label TAN
 #experimental_source brain
 COMMENT This protein is coupled to a G protein and evokes a variety of functions by mediating intracellular signal transduction.
 CLASSIFICATION #superfamily metabotropic glutamate receptor 4
 KEYWORDS G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

FEATURE 1-18
 19-872
 #domain signal sequence #status predicted #label SIG
 #product metabotropic glutamate receptor 2 #status predicted #label MPT

568-590 #domain transmembrane #status predicted #label TR1\
 605-625 #domain transmembrane #status predicted #label TR1\
 637-655 #domain transmembrane #status predicted #label TR1\
 660-700 #domain transmembrane #status predicted #label TR1\
 726-747 #domain transmembrane #status predicted #label TR1\
 761-782 #domain transmembrane #status predicted #label TR1\
 795-819 #domain transmembrane #status predicted #label TR1\
 203,286,338,402, #binding_site carbohydrate (Asn) (covalent) #status predicted\
 347
 601,675,827,837, #binding_site phosphate (Ser) (covalent) #status predicted\
 843
 832 #binding_site phosphate (Thr) (covalent) #status predicted

SUMMARY #length 872 #molecular-weight 95773 #checksum 5740

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 Best Local Similarity 24.7%; Pred. No. 1,866-09;
 Matches 55; Conservative 66; Mismatches 80; Indels 22; Gaps 19;

Db 611 GGVFLCYMTVEFIA-KSTAVCTLRLLGTAFSCVSAALLTNRITATFGARREGAQ 669
 OY 532 ASIFL-FGLDGSFVSEKFEFFELCTVRLIVGTTAGAFATWVHALFKNVK-MK 588

Db 670 RPRFTSPASQVAICLAISGQLLYAAWLVYEA-PGT-GK-ETAPER--REV-V-TL--R 720
 OY 589 K-KIKDKRLVIVGMLIDICLICQAVDPKRRVEKYSMEDEPGRDISIRPLEH 647

Db 721 CNHRDASM-LGSL-AYNYLLAL-CTLYAFKTRKCP-ENFNAKAFIGTWTTCIIMLAF 776
 OY 648 CENITMTITWLGIVAYKGLMLDFGCL-AMETRNVSIPALDSKIGKSVNVMGIMCIIG 706

Db 777 LPIFVTSDDYKVTQTTMCVSSLSGSVVLGCL-FAPRLITLL 818
 OY 707 AAVSFLTRDQPNVQFCIYAVIIFCSTTL-CIYFVPRKL-ITL 747

RESULT 13
 ENTRY JH0562 #type complete
 TITLE metabotropic glutamate receptor 3 precursor - rat
 ORGANISM #formal_name Rattus norvegicus #common_name Norway rat

DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998

ACCESSIONS JH0562
 REFERENCE JH0561
 #authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
 #journal Neuron (1992) 8:169-179
 #title A family of metabotropic glutamate receptors.
 #cross-references MUID:92110002

ACCESSION JH0562
 REFERENCE JH0562
 #authors
 #residues 1-879 #label TAN
 #experimental_source brain
 COMMENT This protein is coupled to a G protein and evokes a variety of functions by mediating intracellular signal transduction.
 CLASSIFICATION #superfamily metabotropic glutamate receptor 4
 KEYWORDS G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

FEATURE 1-22
 23-879
 #domain signal sequence #status predicted #label SIG
 #product metabotropic glutamate receptor 3 #status predicted #label MPT

577-599 #domain transmembrane #status predicted #label TR1\
 614-634 #domain transmembrane #status predicted #label TR1\
 646-664 #domain transmembrane #status predicted #label TR1\
 689-709 #domain transmembrane #status predicted #label TR1\
 735-756 #domain transmembrane #status predicted #label TR1\
 770-791 #domain transmembrane #status predicted #label TR1\
 804-828 #domain transmembrane #status predicted #label TR1\
 209,292,414,439 #binding_site carbohydrate (Asn) (covalent) #status predicted\
 610,845 #binding_site phosphate (Ser) (covalent) #status predicted

SUMMARY #length 879 #molecular-weight 98959 #checksum 5581

Query Match 2.7%; Score 187; DB 2; Length 879;
 Best Local Similarity 34.6%; Pred. No. 3,476-09;
 Matches 28; Conservative 26; Mismatches 26; Indels 1; Gaps 1;

Db 145 VIGSSVSISQVANNLRLEFQIPQISYASATLSKRSKYDFARVPPDFQAKAMEI 204
 OY 130 VFSGVCPSTVSIIESLQGNLVLSFAITPVLAQKKRPYFRTVPDANVNPAILKL 189

Db 205 LRFENMTYVSTVASEGD-YGE 224
 OY 190 LKHQKRVGTITQDVORSE 210

RESULT 14
 ENTRY S49341 #type complete
 TITLE calcium-sensing receptor - human
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 03-Aug-1995

ACCESSIONS S49341; A49419; B49419; C49419
 REFERENCE S49341
 #authors Pearce, S.H.S.; Thakker, R.V.
 #submission submitted to the EMBL Data Library, August 1994
 #accession S49341
 #status preliminary
 #molecule_type DNA
 #residues 1-1078 #label PEA
 #cross-references EMBL:X81086

REFERENCE A49419
 #authors Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi, T.; Seidman, C.E.; Seidman, J.G.
 #journal Cell (1993) 75:1297-1303
 #title Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalcemic hypercalciemia and neonatal severe hyperparathyroidism.
 #cross-references MUID:94094324
 #accession A49419
 #status preliminary
 #molecule_type DNA

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##residues      178-180,'K',182-192 ##label POL
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##note          sequence inconsistent with nucleotide translation
##note          sequence modified after extraction from NCBI backbone
##note          186-Arg mutation is associated with familial
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##status      preliminary
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##residues      289-303 ##label PO2
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##experimental_source family E
##note      sequence modified after extraction from NCBI backbone
##note      298-Lys mutation is associated with familial
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#note	sequence extracted from NCBI backbone (NCBIN:142455)
#accession	C49419

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##residues 788-802 ##label PO3
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#note      sequence extracted from NCBI backbone (NCBIN:142157)
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Query Match	2.7%;	Score 187;	DB 2;	Length 1078;
Best Local Similarity	26.4%;	Pred. No. 3.47e-09;		
Matches	24;	Conservative	34;	Mismatches 33;
			Indels	0;
			Gaps	0;

D6 125 LDECNCSSEHPISTTAVVGAGCGSVSTAIVANLIGLFYIPQVSYASSSSRLSNKNQPSFL 184
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 114 LKAFYDAIKKGPNHLWFGGCGPVSYSIAESIQGMNLVOLSFATTPVLADKKKPYFF 173

Db 185 RTIPNDEHQATAMADIIIEYFRWNVGTIAAD 215
 174 RTVPSDNAVNPAIKLKLLKHQWKRVGTLTQD 204

RESULT	15
ENTRY	A56715
TITLE	#type complete
ORGANISM	calcium receptor (clone pPCar-4.0) - human
DATE	#formal name Homo sapiens #common name man
	19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change
	17-Mar-1999

ACCESSIONS A56715
REFERENCE A56715
#authors Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.; Nemeeth, E.F.; Fuller, F.
#journal J. Biol. Chem. (1995) 270:12919-12925
#title Molecular cloning and functional expression of human parathyroid calcium receptor cDNAs.
#cross-references M0ID:95279439

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#accession      A56715
#status         preliminary
##residues     1-1078 ##label GAR
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##cross-references GB:U02073; NID:q663744; PID:q6583745
glycoprotein; receptor; transmembrane protein
#length 1078 #molecular_weight 120573 #checksum 7868
KEYWORDS
SUMMARY

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Query Match	2.78;	Score 184;	DB 2;	Length 1078;
Best Local Similarity	26.48;	Pred. No. 8.81e-09;		
Matches	24;	Conservative	34;	Mismatches 33;
			Indels	0;
			Gaps	0;

Dd 125 LDFEFCNCSEHIPSTIAVVGATGSGVSTAVALNGLFETYPQVSVAASSRLSNKNOFKSFL 184
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
0y 114 LKAIFYDAIKYGNHLMVFEGCPCPSYSIIAESLOGMNVLQSFATTPTVLADKKRYEFF 173

Db 185 RTIPNDEHQATAMADIIIEFRWNVGTIAAD 215
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 Qy 174 RTVPSDNAVNPAILKLLKHYQWKRVGTLTD 204

Search completed: Wed Apr 19 21:51:26 2000
Job time : 96 secs.


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CC      FILING DATE: 30-DEC-1993
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Parmelee, Steven W.
CC      REGISTRATION NUMBER: 31,990
CC      REFERENCE/DOCKET NUMBER: 13952-18-2
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 206-467-9600
CC      TELEFAX: 415-576-0300
CC      INFORMATION FOR SEQ ID NO: 2:
CC      SEQUENCE CHARACTERISTICS:
CC          LENGTH: 915 amino acids
CC          TYPE: amino acid
CC          TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 915 AA; 102231 MW; 4431664 CN;

Cc      Query Match                3.1%; Score 214; DB 1; Length 915;
Cc      Best Local Similarity 22.9%; Pred.No.3,81e-06;
Cc      Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22.

Dd    597 LAMIGII-ATIEVMATPIRYNDPIVRASGRELISVLTIGIFCY--ITYF-L--MIA- 648
Dy    488 LTIGIMIASAFLEFFN-IKNNOKLTKIKSSPYNNMLIILGGMLSYSASIFLFGLDGSFVSE 546
Dd    649 KPDVAVCSFRRVFLGLGICISYALTLTKNTNIYRIFEDQKKSYAPARLISTSOLATSS 708
Dy    *   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd    547 KTFEELIVRWILLTVGTFAFGAMFAETWVVAIPKRNKK-K-RITDKLLVTGG 603
Dd    709 LISVOLLAGVF-WFEGVDPPNIIID-YD-EHKTMNPDEA-RGVLK-CDITDLOI-ICSL-G 761
Dy    :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd    604 MLILDV-CILICMOAVDPRLRTVEKYSNEPDPADRODISIRPLEHCENTHMTIMLGVIYA 662
Dy    :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd    762 YSILLM-TC-TVYAIAKTGPVENEFENAKPIGFTMYTTCIWMLAFIPIFEQTAAAEKLY 819
Dy    663 YKGILMEGCFLAMPTNRVSIPA-LNSDKICYGMSYVNGIMCIIGAAVSFILRDQPNVQF 721
Dd    820 IOTTILTISMNLASVALGMILMKRYVIIIHPELANOAKRRKF 863
Dy    :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dy    722 C-IVALVI-I-FGSTITLCIVEPKLLITLRPNPDAAATONRRFOF 762

RESULT      4
ID US-08-452-734A-2 STANDARD: PRT; 915 AA.
AC xxxxxx
DX
DY
XX Sequence 2, Application US/08452734A
XX Patent No. 5831047
CC GENERAL INFORMATION:
CC APPLICANT: Segerson, Thomas P.
CC APPLICANT: Kinzie, J. Mark
CC APPLICANT: Mulvihill, Eileen R.
CC APPLICANT: Saugstad, Julie A.
CC APPLICANT: Westbrook, Gary L.
CC TITLE OF INVENTION: L-P4 SENSITIVE GLUTAMATE RECEPTORS
CC NUMBER OF SEQUENCES: 5
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, 8th Floor
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
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CC CC APPLICATION NUMBER: US/08/452,734A  
CC FILING DATE: 30-MAY-1995  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/176,401  
CC FILING DATE: 30-DEC-1993  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Parmelee, Steven W.  
CC REGISTRATION NUMBER: 31,990  
CC REFERENCE/DOCKET NUMBER: 13952-18-1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 206-467-9600  
CC TELEFAX: 415-576-0300  
CC INFORMATION FOR SEO ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 915 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
SQ SEQUENCE 915 AA; 102231 MW; 4431664 CN;  
  
Query Match 3.1%, Score 214, DB 2; Length 915;  
Best Local Similarity 22.9%; Pred. No. 3,81e-06;  
Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22.  
  
Db 597 LAMGII-AITEFWATFIKRNDFTRIVASAGRELSTVLTIGTIFCY--IITF-L---MIA- 648  
QY 488 LTILGMIMASFLEPN-KLNNOKLIMSSSPYMNNLIIILGMLSYASIFLGIDGSFVSE 546  
Dd 649 KPDVAFCFRVFRTGLGMCISYALLTKTNRIYRIFEQGKKSVAPRLISPTSLAITSS 708  
Oy 547 KTFFELICVRKIWLIEVGTTAFGAEMFAKTWVHAHFNVMKK-K-RINDOKLLVIYCG 603  
Db 709 LISVOLLAGVT-WFGVDPPNIID-YD-EHKTMNPEQA-KGVLK-CDTTLQT-ICSL-G 761  
Oy 604 MLIIDL-CILICMOAVDLRRTVKEYSMEDPDPAGRDISIRPLEHCENTHTWTILGIYA 662  
Dd 762 YSILMV-TC-TVAAIKRGVPENFENEKRIGFTINMTTCIYWLAFLIFFEFTAQSARELY 819  
Oy 663 YKGLMLMGCEPLAMEFWNVSIIPA-LNSDKYIGMSVYNVIMCIIGAANVSFLTROPDVQF 721  
Db 820 IOTTLTISMNISASVALGMLYMPRVYIIIPHELNVQRKRKF 863  
Oy 722 C-YVALVT-I-FCSIITLCIFYVERKLIITLRNPDAADQNRRFOF 762  
  
RESULT 5 STANDARD: PRT; 915 AA.  
ID PCr-US94-14989-2  
XX xxxxxx  
DE Sequence 2, Application PC/TUS9414989  
XX Sequence 2, Application PC/TUS9414989  
CC GENERAL INFORMATION:  
CC APPLICANT:  
CC TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS  
CC NUMBER OF SEQUENCES: 3  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: floppy disk  
CC OPERATING SYSTEM: IBM PC compatible  
CC SOFTWARE: PC-DOS/MS-DOS  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCr/TUS94/14989  
CC FILING DATE:  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/176,401  
CC FILING DATE: 30-DEC-1993  
CC ATTORNEY/AGENT INFORMATION:
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CC LENGTH: 879 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 879 AA; 98878 MW; 4241110 CN;

Query Match          2.7%; Score 187; DB 3; Length 879;
Best Local Similarity 34.6%; Pred. No. 2,66e-04;
Matches 28; Conservative 26; Mismatches 26; Indels 1; Gaps 1

Db      145 VIGGVSSVSTQVANLFLFDLPDQSVASTAKLSDKSRIRYFATVPDPDYQAKMAEI 204
Oy      130 VFEGVCPEVSTIIASLGMDNLVOLSFSAATPPVLADKKRYFFRTVPSDNAVNPAILKL 189
Db      205 LRFENMIVTYSVASEGD-YGE 224
Oy      190 LKHVMKRVGTLTQDVQRFE 210

RESULT           9
ID US-08-072-574-2 STANDARD; PRT; 905 AA.
XX xxxxxx
DE Sequence 2, Application US/08072574
XX
CC Sequence 2, Application US/08072574
CC Patent No. 5521297
CC GENERAL INFORMATION:
CC APPLICANT: Daggett, Lorrie
CC APPLICANT: Ellis, Steven B.
CC APPLICANT: Liaw, Chen
CC APPLICANT: Pontsier, Aaron
CC TITLE OF INVENTION: HUMAN MATABOTROPIC GLUTAMATE RECEPTORS,
CC TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
CC NUMBER OF SEQUENCES: 13
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
CC STREET: 444 South Flower Street, Suite 2000
CC CITY: Los Angeles
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 00719
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/072,574
CC FILING DATE: 19930604
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Reiter, Stephen E.
CC REGISTRATION NUMBER: 31,192
CC REFERENCE/DOCKET NUMBER: P41 9383
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 213-622-7700
CC TELEFAX: 213-489-4210
CC INFORMATION FOR SEO ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 905 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 905 AA; 101396 MW; 4448023 CN;

Query Match          2.7%; Score 189; DB 1; Length 905;
Best Local Similarity 36.1%; Pred. No. 1.95e-04;
Matches 26; Conservative 22; Mismatches 24; Indels 0; Gaps 0;
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Db      159 VIGAGSSSAVLQVONLQLFPIPLIAASATSIDSDKLTLYFLRVYPSDTLQARMLDI 218
|:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|:
Qy      130 VFGEVCPSVTIITLESIQGNMLVLSRAITTPVLADKKKTFPFRPVSPDNANPALIKL 189
|:~| |~|: |:~| |~|: |:~| |~|: |:~| |~|: |:~| |~|: |:~| |~|: |:~| |~|: |:~|

Db      219 VKRYNMITYVSAY 230
|:~| |~|: |:~| |~|: |:~| |~|: |:~| |~|: |:~| |~|: |:~| |~|: |:~| |~|: |:~|

Qy      190 LKHYYMKRKGTL 201
|:~| |~|: |:~| |~|: |:~| |~|: |:~| |~|: |:~| |~|: |:~| |~|: |:~| |~|: |:~|

RESULT 10 STANDARD; PRT; 906 AA.
ID     PC1-US91-09422-17
AC     xxxxxx
DT
XX
XX
Sequence 17, Application PC/TUS9109422
CC
DE
XX
Sequence 17, Application PC/TUS9109422
CC
GENERAL INFORMATION:
CC   APPLICANT: Mulvihill, Eileen R.
CC   APPLICANT: Hagen, Frederick S.
CC   APPLICANT: Houamed, Khalid M.
CC   APPLICANT: Almers, Wolfhard
CC   TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
CC   NUMBER OF SEQUENCES: 33
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Townsend and Townsend
CC   STREET: One Market Plaza, Steuart Street Tower
CC   CITY: San Francisco
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94105-1492
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, Version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: PCT/US91/09422
CC   FILING DATE: 19911212
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: US 07/672,007
CC   FILING DATE: 18-MAR-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: US 07/648,481
CC   FILING DATE: 30-JAN-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: US 07/626,806
CC   FILING DATE: 12-DEC-1990
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Parmelee, Steven W.
CC   REGISTRATION NUMBER: 31,990
CC   REFERENCE/DOCKET NUMBER: 13952-6PC
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (206) 467-9600
CC   TELEFAX: (415) 543-5043
CC   INFORMATION FOR SEQ ID NO: 17:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 906 amino acids
CC   TYPE: AMINO ACID
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
CC   SEQUENCE 906 AA; 101637 MW; 4413609 CN;
SQ
Query Match 2.7%; Score 186; DB 4; Length 906;
Best Local Similarity 36.1%; Pred. No. 3,1le-04;
Matches 26; Conservative 21; Mismatches 25; Indels 0; Gaps 0.
QY      159 VIGPSSSVALQVONLQLFDIPQIALTSIDSKLTLYFLRVYPSDTLQARMLDI 218
|:~| |:~| |:~| |:~| |:~| |:~| |:~| |:~| |:~| |:~| |:~| |:~| |:~| |:~| |:~|
130 VFGEVCPSVTSTIASISLGQMWLVQSFAITFPVLADKKKTFPFRPVSDNANPALIKL 189

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	Db	219 VKRYNWTYVSAY 230
		: : :::
QY	190 LKHYYMKRVTGL 201	
	RESULT 11	
XX	ID US-08-486-270-2	STANDARD: PRT; 906 AA.
AC	xxxxxx	
XX		
DT		
XX		
DE	Sequence 2, Application US/08486270	
CC	Patent No. 5807689	
CC		
CC	GENERAL INFORMATION:	
CC	APPLICANT: Daggett, Lorrie	
CC	APPLICANT: Ellis, Steven B.	
CC	APPLICANT: Liaw, Chen	
CC	APPLICANT: Pontsler, Aaron	
CC	APPLICANT: Johnson, Edwin C.	
CC	APPLICANT: Hess, Stephen D.	
CC	TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS	
CC	TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF	
CC	NUMBER OF SEQUENCES: 13	
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark	
CC	STREET: 444 South Flower Street, Suite 2000	
CC	CITY: Los Angeles	
CC	STATE: CA	
CC	COUNTRY: USA	
CC	ZIP: 90071	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: Floppy disk	
CC	COMPUTER: IBM PC compatible	
CC	OPERATING SYSTEM: PC-DOS/MS-DOS	
CC	SOFTWARE: Patentin Release #1.0, Version #1.25	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER: US/08/486, 270	
CC	FILING DATE: 02-JUN-1994	
CC	CLASSIFICATION: 435	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: US 08/072, 574	
CC	FILING DATE: 04-JUN-1993	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME: Reltter, Stephen E.	
CC	REGISTRATION NUMBER: 31,192	
CC	REFERENCE/DOCKET NUMBER: FP41 9772	
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE: 619-546-4737	
CC	TELEFAX: 619-546-9392	
CC	INFORMATION FOR SEQ ID NO: 2:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH: 906 amino acids	
CC	TYPE: amino acid	
CC	TOPOLOGY: linear	
CC	MOLECULE TYPE: protein	
SQ	SEQUENCE 906 AA; 10192 MW; 4407237 CN;	
	Query Match 2.7%; Score 186; DB 1; Length 906;	
	Best Local Similarity 36.1%; Pred.No.3,11e-04;	
	Matches 26; Conservative 21; Mismatches 25; Indels 0; Gaps 0;	
Db	159 VIGPESSVAIQVONTLQFDIPQIAISATSIDSKTKTYEFLRAVPSPDLARAMD I 218	
	: : : :: : : : : :	
QY	130 VFGGCPCSVTSILIESLOGMNIOLSFATPTPLADKKKPYFFRPVPSDNAANPALIKL 189	
	: : :::	
Db	219 VKRYNWTYVSAY 230	
	: : :::	
QY	190 LKHYYMKRVTGL 201	

RESULT 12
ID US-08-367-264-2 STANDARD: PRT: 906 AA.
XX
AC xxxxxx
XX
XX
DE Sequence 2, Application US/08367264
XX
CC Sequence 2, Application US/08367264
CC Patent No. 6001581
CC GENERAL INFORMATION:
CC APPLICANT: Daggett, Lorrie
CC APPLICANT: Ellis, Steven B.
CC APPLICANT: Liaw, Chen
CC APPLICANT: Pontsler, Aaron
CC APPLICANT: Johnson, Edwin C.
CC APPLICANT: Hess, Stephen D.
CC TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
CC TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
CC NUMBER OF SEQUENCES: 13
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pretly, Schroeder, Brueggemann & Clark
CC STREET: 444 South Flower Street, Suite 2000
CC CITY: Los Angeles
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/367,264
CC FILING DATE: 02-JUN-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/072,574
CC FILING DATE: 04-JUN-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Reiter, Stephen E.
CC REGISTRATION NUMBER: 31,192
CC REFERENCE/DOCKET NUMBER: FP41 9772
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-546-4737
CC TELEFAX: 619-546-9392
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 906 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 906 AA; 101292 MW; 4407237 CN;
SQ
Query Match 2.7%; Score 186; DB 3; Length 906;
Best Local Similarity 36.1%; Pred. No. 3.11e-04;
Matches 26; Conservative 21; Mismatches 25; Indels 0; Gaps 0;
Db 159 VIGPGSSVAIOYONLLOFDIPQIAYSATSIDLSDKTLRYKFLRVVPSDQLQARMLDI 218
Y 130 VFGVCPSPVTSIAESLOGMNLVQLSFAATTPVLADKKKYPFFKRVPSDNVNPAILKL 189
Db 219 VKRYNMTYVSAY 230
Y 190 LKHQMKRVGTL 201
RESULT 13
ID US-08-687-289A-7 STANDARD: PRT: 1056 AA.
XX
AC xxxxxx

XX
DT
XX
DE Sequence 7, Application US/08687289A
XX
CC Sequence 7, Application US/08687289A
CC Patent No. 5981195
CC GENERAL INFORMATION:
CC APPLICANT: Fuller, Forrest H.
CC APPLICANT: Krapcho, Karen J.
CC APPLICANT: Hamnerland, Lance G.
CC TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR
CC TITLE OF INVENTION: IDENTIFYING COMPOUNDS ACTIVE AT
CC TITLE OF INVENTION: METABOTROPIC GLUTAMATE RECEPTORS AND
CC TITLE OF INVENTION: THE USE OF SUCH COMPOUNDS IN THE
CC TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS
CC NUMBER OF SEQUENCES: 8
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: 633 West Fifth Street
CC CITY: Suite 4700
CC STATE: California
CC COUNTRY: U.S.A.
CC ZIP: 90071-2066
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB
CC MEDIUM TYPE: storage
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: IBM P.C. DOS 5.0
CC SOFTWARE: Fastseq for Windows 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/687,289A
CC FILING DATE: July 25, 1996
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 60/001,526
CC FILING DATE: July 26, 1995
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Warburg, Richard J.
CC REGISTRATION NUMBER: 32,327
CC REFERENCE/DOCKET NUMBER: 220/004
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1056 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: Protein
CC SEQUENCE 1056 AA; 117663 MW; 5988966 CN;
SQ
Query Match 2.7%; Score 186; DB 2; Length 1056;
Best Local Similarity 36.1%; Pred. No. 3.11e-04;
Matches 26; Conservative 21; Mismatches 25; Indels 0; Gaps 0;
Db 159 VIGPGSSVAIOYONLLOFDIPQIAYSATSIDLSDKTLRYKFLRVVPSDQLQARMLDI 218
Y 130 VFGVCPSPVTSIAESLOGMNLVQLSFAATTPVLADKKKYPFFKRVPSDNVNPAILKL 189
Db 219 VKRYNMTYVSAY 230
Y 190 LKHQMKRVGTL 201
RESULT 14
ID US-08-687-289A-8 STANDARD: PRT: 1056 AA.
XX
AC xxxxxx

XX
DE
XX
XX
Sequence 8, Application US/08687289A
CC
XX
Sequence 8, Application US/08687289A
CC
Patent No. 5981195
CC
GENERAL INFORMATION:
CC
APPLICANT: Fuller, Forrest H.
CC
APPLICANT: Krapcho, Karen J.
CC
APPLICANT: Hammerland, Lance G.
CC
TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR
CC
TITLE OF INVENTION: IDENTIFYING COMPOUNDS ACTIVE AT
CC
TITLE OF INVENTION: METABOTROPIC GLUTAMATE RECEPTORS AND
CC
TITLE OF INVENTION: THE USE OF SUCH COMPOUNDS IN THE
CC
TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS
CC
NUMBER OF SEQUENCES: 8
CC
CORRESPONDENCE ADDRESS:
CC
ADDRESSEE: Lyon & Lyon
CC
STREET: 633 West Fifth Street
CC
STREET: Suite 4700
CC
CITY: Los Angeles
CC
STATE: California
CC
COUNTRY: U.S.A.
CC
ZIP: 90071-2066
CC
COMPUTER READABLE FORM:
CC
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
CC
MEDIUM TYPE: Storage
CC
COMPUTER: IBM Compatible
CC
OPERATING SYSTEM: IBM P.C. DOS 5.0
CC
SOFTWARE: FastSeq for Windows 2.0
CC
CURRENT APPLICATION DATA:
CC
APPLICATION NUMBER: US/08/687,289A
CC
FILING DATE: July 25, 1996
CC
CLASSIFICATION: 435
CC
PRIOR APPLICATION DATA:
CC
APPLICATION NUMBER: 60/001,526
CC
FILING DATE: July 26, 1995
CC
ATTORNEY/AGENT INFORMATION:
CC
NAME: Warburg, Richard J.
CC
REGISTRATION NUMBER: 32,327
CC
REFERENCE/DOCKET NUMBER: 220/004
CC
TELECOMMUNICATION INFORMATION:
CC
TELEPHONE: (213) 489-1600
CC
TELEFAX: (213) 955-0440
CC
TELEX: 67-3510
CC
INFORMATION FOR SEQ ID NO: 8:
CC
SEQUENCE CHARACTERISTICS:
CC
LENGTH: 1056 amino acids
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TYPE: amino acid
CC
STRANDEDNESS: single
CC
TOPOLOGY: linear
CC
MOLECULE TYPE: Protein
CC
SEQUENCE 1056 AA; 117600 MW; 5991921 CN;
SQ
Query Match 2.7%; Score 186; DB 2; Length 1056;
Best Local Similarity 36.1%; Pred. No. 3.11e-04;
Matches 26; Conservative 21; Mismatches 25; Indels 0; Gaps 0;
Db 159 VIGPSSVAIQVONLLQFLDPIQVYSATSDLSKTLKYLRYVPSDTLQARAMD I 218
QY 130 VFGGVCPSVSTIASESLQGNVLQSLFAATTPVLADKKRYPFFRTVPSDNAVNPAILKL 189
Db 219 VKRYNMTYVSAY 230
QY 190 LKHVQMKRVGTL 201
RESULT 15
ID US-08-687-289A-5 STANDARD; PRT; 1058 AA.
XX
C
xxxxxx

XX
DE
XX
XX
Sequence 5, Application US/08687289A
CC
XX
Sequence 5, Application US/08687289A
CC
Patent No. 5981195
CC
GENERAL INFORMATION:
CC
APPLICANT: Fuller, Forrest H.
CC
APPLICANT: Krapcho, Karen J.
CC
APPLICANT: Hammerland, Lance G.
CC
TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR
CC
TITLE OF INVENTION: IDENTIFYING COMPOUNDS ACTIVE AT
CC
TITLE OF INVENTION: METABOTROPIC GLUTAMATE RECEPTORS AND
CC
TITLE OF INVENTION: THE USE OF SUCH COMPOUNDS IN THE
CC
TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS
CC
NUMBER OF SEQUENCES: 8
CC
CORRESPONDENCE ADDRESS:
CC
ADDRESSEE: Lyon & Lyon
CC
STREET: 633 West Fifth Street
CC
STREET: Suite 4700
CC
CITY: Los Angeles
CC
STATE: California
CC
COUNTRY: U.S.A.
CC
ZIP: 90071-2066
CC
COMPUTER READABLE FORM:
CC
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
CC
MEDIUM TYPE: Storage
CC
COMPUTER: IBM Compatible
CC
OPERATING SYSTEM: IBM P.C. DOS 5.0
CC
SOFTWARE: FastSeq for Windows 2.0
CC
CURRENT APPLICATION DATA:
CC
APPLICATION NUMBER: US/08/687,289A
CC
FILING DATE: July 25, 1996
CC
CLASSIFICATION: 435
CC
PRIOR APPLICATION DATA:
CC
APPLICATION NUMBER: 60/001,526
CC
FILING DATE: July 26, 1995
CC
ATTORNEY/AGENT INFORMATION:
CC
NAME: Warburg, Richard J.
CC
REGISTRATION NUMBER: 32,327
CC
REFERENCE/DOCKET NUMBER: 220/004
CC
TELECOMMUNICATION INFORMATION:
CC
TELEPHONE: (213) 489-1600
CC
TELEFAX: (213) 955-0440
CC
TELEX: 67-3510
CC
INFORMATION FOR SEQ ID NO: 5:
CC
SEQUENCE CHARACTERISTICS:
CC
LENGTH: 1058 amino acids
CC
TYPE: amino acid
CC
STRANDEDNESS: single
CC
TOPOLOGY: linear
CC
MOLECULE TYPE: Protein
CC
SEQUENCE 1058 AA; 118709 MW; 5901398 CN;
SQ
Query Match 2.7%; Score 186; DB 2; Length 1058;
Best Local Similarity 36.1%; Pred. No. 3.11e-04;
Matches 26; Conservative 21; Mismatches 25; Indels 0; Gaps 0;
Db 159 VIGPSSVAIQVONLLQFLDPIQVYSATSDLSKTLKYLRYVPSDTLQARAMD I 218
QY 130 VFGGVCPSVSTIASESLQGNVLQSLFAATTPVLADKKRYPFFRTVPSDNAVNPAILKL 189
Db 219 VKRYNMTYVSAY 230
QY 190 LKHVQMKRVGTL 201
Search completed: Wed Apr 19 22:07:42 2000
Job time : 24 secs.


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Oy 162 VLADKKKKYFFRTVPSPDNVNPALILKLKHQMKRVGTLTLDQVRFSEVKNDLTGVLG 221
Db 216 AGIEITTFQSFSPDPANVVKMLKRODARIIVGLFETEARVFEVYKRELFGKKYVWL 275
Oy 222 EDIEISDTESFSDPCTSVKKIKGNDVRIILGFDONMAAKVFCACAEENNYGSKYOMII 281
Db 276 IGVYADNMNF-KIY-DP-SINCTVDEMTAEVGHITTEIVMLNPANTRSISIMTQSOEVEK 332
Oy 282 PGWEPSPMEOVHTEANSSRCLRNLAAMGTYGVDFEPLISKOITISKTPOQY-ER 340
Db 333 LTKLRKHPDEETGFOEAPLAYDAIMALALANKTSGG--GGRSGVRLDEPNYNNQITTD 390
Oy 341 EYNN-KRSGVPSKFH-G-YAYDGIWIAKTQORAMETLHAASRHORIODEPNYDHTLGR 397
Db 391 OIYRAMNSSFEVSGHAYVFPDASSRRAMWTILEOLGSGYKIKGYSTKDDLSW-SKT 449
Oy 398 IILNMMNTEFEGYGVVVF-RNGERMGTIKFTQFOSREKVEYNAVAFTLEINDTI 456
Db 450 KWIIGSPADQTLVTKTRFSLQKLEISVSLSGIYLAIVVCLSPFNYSNHYRIONSQ 509
Oy 457 RFQSEFPKDKTIIIEQLRKISLPLSYLSLALTILGIMASAFLEFNKRNQKLIKMS 516
Db 510 PNLNMLTAVGCSLAAVFPGLDGYHIGNQPFVCOARLMLLGLGSLGYSMTKXW 569
Oy 517 PYMNLILIGMLSYASIFLFGDGSFSEKTFELCTVMTLVGYTAFGAMFAKTW 576
Db 570 WYHIVFTKKEKKERKTLPEMKLYATYGLLVGMVLTIAWQYVDPDLHRTIEFAKEP 629
Oy 577 RVHAIF--KNVKKM-KKIIIDOKLVIYVGMILLDCLICQWADVPLRRTVERKYSMPD 633
Db 630 KEDIVSILIPOLEHSCSRKMTWLGIFGYGKLLILGLIFLAYETKSVSTEKINDHRAV 689
Oy 634 PAGROISIRPLEHCEHNHTIMGLIYAYKGLMLKECFLAMETRNVSIPALNDSKTYG 693
Db 690 MAIYVAVLCITAPVTMLSSQDAFAFASLAIVFSSYITLVLFVPMKRLITRGE 748
Oy 694 MSYVWVGIMCITGAIVSFLTRDQPNVQFCIVALYIIFCSTITLCIVFVKLITLRTNPD 752

RESULT 2
ID W40118 standard; Protein; 844 AA.
AC W40118;
DT 03-JUN-1998 (first entry)
DE Rat GABA-BR1b receptor protein.
KW Gamma-aminobutyric acid; GABA-BR1b receptor; rat; brain; agonist;
  inhibitory neurotransmitter; peripheral nervous system; antagonist;
  treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
  epilepsy; cognitive function.
OS Rattus norvegicus.
PN MO9746675-A1.
PD 11-DEC-1997.
PF 19-MAR-1997; E01370.
PR 22-NOV-1996; US-756091.
PR 30-MAY-1996; US-655716.
PA (NOVS ) NOVARTIS AG.
PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ.
  WPLI: 98-042183/04.
DR N-PSDB; V10266.
DR Purified GABA-B receptor or receptor protein - and antagonists of
  these which may be useful in treating nervous system disorders
PT Claim 4; Page 74-79; 108pp; English.
CC This sequence represents a novel rat GABA-B receptor protein.
  GABA-BR1b (gamma-aminobutyric acid) is the major inhibitory
  neurotransmitter found in the brain and peripheral nervous system
  and this receptor may be used for the identification of GABA-B
  receptor agonists and antagonists. Such proteins may be used in
  treatment of dementia, depression, anxiety, epilepsy, spasticity,
  bronchial inflammation or asthma or to improve cognitive function.
  GABA-B receptor ligands and probes derived from this sequence can be
  used to assay for GABA-B receptors or DNA encoding them.
SQ Sequence 844 AA;

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Query Match 24.5%; Score 1690; DB 1; Length 844;

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Best Local Similarity 35.4%; Pred. No. 1,18e-124;
Matches 268; Conservative 194; Mismatches 271; Indels 23; Gaps 21;

Db 2 GREGCPPTVGMPLPLLVMAAGVAPYMAWASHPLRPHRVPPHPSSEKRAVYICAL-PP 60
Oy 11 PPPPPPPPPARILLILLPL-LLPL-APGAWMAKAPR-PP-PSSPLSI-MGIMBLT 65
Db 61 MSGWPG-GOACOPAVEMALEVDNSRDLIPDYELKIHJHDSKCPGQATKYLEYELND 119
Oy 66 KEVAKSGISGRVLPVLELIEORNE-SILRPFLDLRLYTECDNAGLKAFTAIKYG 124
Db 120 PIKIIIMP-CSSYSTVAEARMNLIVLSYSSSPALNSRQPEFTFRHPASFLANP 178
Oy 125 PNLIAVFGVCPVSTSIILAESLOGMNLVOLSPAATPVLDKKKYFFRTVPSPDNVNP 184
Db 179 TRVKEEKGKKKIATIOOTTEVFTSLDDLEERKKEAGIEITTFQSFSDPNAVVKLK 238
Oy 185 AILKLKHQMKRVGTLTDVORFSEVRNDLTGVLDGEDIESTESFSDPCTSVKKIK 244
Db 239 RODARIIVGLFETEARKEVYKRELFGKKYVWFLIGYADNMNF-KTY-DP-SINCTV 295
Oy 245 GNDVRIILGOFDONMAAKVPCACAEENMTGSKYQWIIIPGWEPSPMEOVHTEANSSRCLR 304
Db 296 EEMTEAVEGHITTEIVMLNPANTRSISIMTQSOEVEKTLKRLKHPDEETGFOEAPLAY 355
Oy 305 KNLLAMEGYIGVDFEPLSKQIKTISKTPOQY-EREYNN-KRSGVPSKFH-G-YAYD 360
Db 356 AIALALANKTSGG--GGRSGVRLDEPNYNNQITDQIYRAMNSSFEVSGHAYVFPDAS 413
Oy 361 GIWIVIAKTQORAMETLHAASRHORIODEPNYDHTLGRILNMMNTEFEGYGVVVF-RN 419
Db 414 GSRMANTLIELOGSGYKIKGYDSTKDDLSW-SKTDKWIIGSPADQTLVTKTRFSLQ 472
Oy 420 GERMGTIKFTQFODSREKVKGEYNAVADLLEIINDIRROGSEPPDKTIIIEQLRKISL 479
Db 473 KLEISVSLSGIYLAIVVCLSPFNYSNHYRIONSQPNLNLITAVGCSLAAVFPGL 532
Oy 480 PLYSILSALTILGIMASAFLEFNKRNQKLIKMSPYMNLILIGMLSYASIFLEGL 539
Db 533 DGYHIGRSOPFPVCOARLMLLGLGSLGYSMTKXWYHIVFTKKEKKERKTLPEPK 592
Oy 540 DGSEFSEKTFELCTVMTLVGYTAFGAMFAKTWRVHAIF--KNVKKM-KKIIIDOK 596
Db 593 LVAFTVGLVGMVLTIAWQYVDPDLHRTIETFAKEPKEDIVSILIPOLEHSCSRKMTW 652
Oy 597 LVIYVGMILLDCLICQWADVPLRRTVERKYSMEDPAGROISIRPLEHCEHNHTIM 656
Db 653 LGIFYGKGLLLILGLIFLAYETKSVSTEKINDHRAVGMALYVAVLCITAPVTMLSSQ 712
Oy 657 LGIYVAYKGLMLKECFLAMETRNVSIPALNDSKTYGMSYVWVGIMCITGAIVSFLTRDQ 716
Db 713 QDAFAFASLAIVFSSYITLVLFVPMKRLITRGE 748
Oy 717 PNVOFCIVALYIIFCSTITLCIVFVKLITLRTNPD 752

RESULT 3
ID W40117 standard; Protein; 793 AA.
AC W40117;
DT 03-JUN-1998 (first entry)
DE Human GABA-BR1a/b receptor protein.
KW Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;
  inhibitory neurotransmitter; peripheral nervous system; antagonist;
  treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
  epilepsy; cognitive function.
OS Homo sapiens.
PN MO9746675-A1.
PD 11-DEC-1997.
PF 19-MAR-1997; E01370.
PR 22-NOV-1996; US-756091.
PR 30-MAY-1996; US-655716.
PA (NOVS ) NOVARTIS AG.
PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ.

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DR WPI: 98-042183/04.
DR N-PSDB: V10265.
PT Purified GABA-B receptor or receptor protein - and antagonists of
PT these which may be useful in treating nervous system disorders
PS Claim 4; Page 62-67; 108pp; English.
CC This sequence represents a novel human GABA-B receptor protein,
CC GABA-BR1A/D. GABA (gamma-aminobutyric acid) is the major inhibitory
CC neurotransmitter found in the brain and peripheral nervous system
CC and this receptor may be used for the identification of GABA-B
CC receptor agonists and antagonists. Such proteins may be used in
CC treatment of dementia, depression, anxiety, epilepsy, spasticity,
CC bronchial inflammation or asthma or to improve cognitive function.
CC GABA-B receptor ligands and probes derived from this sequence can be
CC used to assay for GABA-B receptors or DNA encoding them.
SQ Sequence 793 AA;

Query Match 24.4%; Score 1687; DB 1; Length 793;
Best Local Similarity 36.2%; Pred. No. 2,08e-124;
Matches 249; Conservative 180; Mismatches 243; Indels 16; Gaps 14;

Db 17 GACGCPAVALMALADVNSRRDILPDYELKLIHSDKCDPGQATKYLYELLNDPIKILMP 76
QY 74 GRGVLPAYELAIQIIRNE-SLIRPYFLDLRLDYEDCNAGKAKFYDAIKYGNHLMWFG 132
Db 77 G-CSSVSTLVAAARMNLIVLSYSSSPALSNRQFPPTFFRTHPSATLHNPTRYKLEPK 135
QY 133 GVCPSVTSIIASLQGMNLVOLSPFATTPVLADKKRYFFFTVPSDNAVNALIKLKH 192
Db 136 WGMKRIATIQOTTEVFTSLDLEERVKAGIEITFRGSPFSDPAVPVKNLRDARIIV 195
QY 193 YQMKRGTLTQDVQRFSEVRNDLTGVLGEDIEISDTSFSDNPTCSYKLGKNVRIIL 252
Db 196 GLPYETEARKVCYKERRLPFGKKYWFLLIGVADNMF-KTY-DP-SINCTYDEMTAE 252
QY 253 GQPDQMAAKVFCACAEENMGSKYQWILPGMYEBSMWEQVHTPANSRCLRNILAME 312
Db 253 GHITTEIYMLNPANRISISNMTSOEFVEKLRKLRHRETEGGQAPAPAYADAMALALA 312
QY 313 GYGVDFEFLSKQITIGSKTPQY-EREYNN-KRSGVPSKPH-G-YAIDGIVIAIAT 368
Db 313 LNKTSGG--GGRSGVRLDEPNYNNQITDQIYRAMNSSFEVSGHVAFDASGRMAWTL 370
QY 369 LQRAMETTLHASSRHRIQDFNYTDHILGRILINMANETNFEVTCQVYF-RNGERMGTIK 427
Db 371 IEQLOGGSYKKIIGYDSTKDLISW-SKTDKMGSPPADQTVIKTERLSQKLEISVS 429
QY 428 FTQFQDSREVKVEYNAAVDLEIINDTIRFGQSEPPKDKTILIEQLRKISLPLYSILSA 487
Db 430 LSSIGIYLAIVCLSFENIYNSHRYIYQNSQPNLNLTAAGCSLAALAVFLGIDGYHIGRN 489
QY 488 LTIILGIMASAPLEFNIKRNOKLIKMSSPYNNLLILGMLSTASIFLFGIDGSFVSEK 547
Db 490 QPPEVCQARMLMLGIFSGISGSMETKIWWHTVFTKKEKKEMRKTLLEPKLYATVGL 549
QY 548 TFEITLCYRTWILTYGTTAFGAMFAKTRVHAIF--KNVYMK-KKIIKQKLLVIVGGM 604
Db 550 VGMADVTLAIWQIDPLRITETFAKEEPKEDIVSLIQLEHSGSRKNNTLGLIFYGK 609
QY 605 LLIIDLCILICQWADVPLRITVEKYSMEPPDAGDISIRPLEHCENTHMTWIGIYAYK 664
Db 610 GLLILGIFLAYETKSVSTREKINDHRAVGMATYNAVLCILITAPVTMILSSOODAAFAFA 669
QY 665 GILMLFGCLAMETRNVSIPALNDSKYIGMSYVNGIMKIIIGAAVSFLTRDQPNVOFCIV 724
Db 670 STAIYVSSTITLVYFVPMRRLITRGE 697
QY 725 ALVIIFCSTITLCIVFVPKLITLRTMPD 752

RESULT 4
ID W40116 standard; Protein; 960 AA.
AC W40116;
DT 03-JUN-1998 (first entry)

DE Rat GABA-BR1a receptor protein.
KW Gamma-aminobutyric acid; GABA-BR1a receptor; rat; brain; agonist;
KW inhibitory neurotransmitter; peripheral nervous system; antagonist;
KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
KW epilepsy; cognitive function.
OS Rattus norvegicus.
PN M09746675-A1.
PD 11-DEC-1997.
PE 19-MAR-1997; E01370.
PR 22-NOV-1996; US-756091.
PR 30-MAY-1996; US-655716.
PI Bettler B, Bitliger H, Froestl W, Kaupmann K, Mickel SJ.
DR WPI: 98-042183/04.
DR N-PSDB: V10264.
PT Purified GABA-B receptor or receptor protein - and antagonists of
PT these which may be useful in treating nervous system disorders
PS Claim 4; Page 50-56; 108pp; English.
CC This sequence represents a novel rat GABA-B receptor protein,
CC GABA-BR1a. GABA (gamma-aminobutyric acid) is the major inhibitory
CC neurotransmitter found in the brain and peripheral nervous system
CC and this receptor may be used for the identification of GABA-B
CC receptor agonists and antagonists. Such proteins may be used in
CC treatment of dementia, depression, anxiety, epilepsy, spasticity,
CC bronchial inflammation or asthma or to improve cognitive function.
CC GABA-B receptor ligands and probes derived from this sequence can be
CC used to assay for GABA-B receptors or DNA encoding them.
SQ Sequence 960 AA;

Query Match 24.4%; Score 1682; DB 1; Length 960;
Best Local Similarity 36.2%; Pred. No. 5,39e-124;
Matches 249; Conservative 178; Mismatches 245; Indels 16; Gaps 14;

Db 184 GACGCPAVALMALADVNSRRDILPDYELKLIHSDKCDPGQATKYLYELLNDPIKILMP 243
QY 74 GRGVLPAYELAIQIIRNE-SLIRPYFLDLRLDYEDCNAGKAKFYDAIKYGNHLMWFG 132
Db 244 G-CSSVSTLVAAARMNLIVLSYSSSPALSNRQFPPTFFRTHPSATLHNPTRYKLEPK 302
QY 133 GVCPSVTSIIASLQGMNLVOLSPFATTPVLADKKRYFFFTVPSDNAVNALIKLKH 192
Db 303 WGMKRIATIQOTTEVFTSLDLEERVKAGIEITFRGSPFSDPAVPVKNLRDARIIV 362
QY 193 YQMKRGTLTQDVQRFSEVRNDLTGVLGEDIEISDTSFSDNPTCSYKLGKNVRIIL 252
Db 363 GLPYETEARKVCYKERRLPFGKKYWFLLIGVADNMF-KTY-DP-SINCTYDEMTAE 419
QY 253 GQPDQMAAKVFCACAEENMGSKYQWILPGMYEBSMWEQVHTPANSRCLRNILAME 312
Db 420 GHITTEIYMLNPANRISISNMTSOEFVEKLRKLRHRETEGGQAPAPAYADAMALALA 479
QY 428 FTQFQDSREVKVEYNAAVDLEIINDTIRFGQSEPPKDKTILIEQLRKISLPLYSILSA 487
Db 480 LNKTSGG--GGRSGVRLDEPNYNNQITDQIYRAMNSSFEVSGHVAFDASGRMAWTL 537
QY 369 LQRAMETTLHASSRHRIQDFNYTDHILGRILINMANETNFEVTCQVYF-RNGERMGTIK 427
Db 538 IEQLOGGSYKKIIGYDSTKDLISW-SKTDKMGSPPADQTVIKTERLSQKLEISVS 596
QY 428 FTQFQDSREVKVEYNAAVDLEIINDTIRFGQSEPPKDKTILIEQLRKISLPLYSILSA 487
Db 597 LSSIGIYLAIVCLSFENIYNSHRYIYQNSQPNLNLTAAGCSLAALAVFLGIDGYHIGRN 656
QY 488 LTIILGIMASAPLEFNIKRNOKLIKMSSPYNNLLILGMLSTASIFLFGIDGSFVSEK 547
Db 657 QPPEVCQARMLMLGIFSGISGSMETKIWWHTVFTKKEKKEMRKTLLEPKLYATVGL 716
QY 548 TFEITLCYRTWILTYGTTAFGAMFAKTRVHAIF--KNVYMK-KKIIKQKLLVIVGGM 604
Db 717 VGMADVTLAIWQIDPLRITETFAKEEPKEDIVSLIQLEHSGSRKNNTLGLIFYGK 776
QY 605 LLIIDLCILICQWADVPLRITVEKYSMEPPDAGDISIRPLEHCENTHMTWIGIYAYK 664

Db 588 AVLPFLAVVG-IAATLEVVITFVRKNDPTIVKASGRELSTVLLAGIFLCYATTEL--M- 643
 OY 483 SLISA-LTILGIMASAFLEFN-INKRNOKLIKSSPYMNNLITLIGMISYASIFLEGLD 540
 Db 644 ---IAEPDLGT-CSLRRIEFLGMSISYALLTKTNRIYRIFEOGRSAPFISPASQ 699
 OY 541 GSPFVSEKTEFTLCTVRWILLVGTTFAGFAKTMVHAIFKNVK--MKK-KIIOQKL 597
 Db 700 LAIFSLISLQI-LGICWFWVPSHSVVD-FODQRTLDPR-PA-RGVLK-CDISDLSL- 753
 OY 598 LVIYVGMILLDLCILIC-WQAVDPLRTVEKYSMEPDPAIRODISIPLEHCENTHMTIIV 656
 Db 754 ICLL-GYSMLLMV-TC-TVYAIKTRGVPEFNEAKRPIGFMTYTTCIYWLAFIPIFGTSQ 810
 OY 657 LGIYVAAKGLIMLEFGCLAMETRNVSIP-ALNDSKYIGMSVYVNGIMCIIIGAAVSFLTRD 715
 Db 811 SADKLXIQTTLTIVSVLSASVSLGMLYMPKYYIILFHPQONVPRK 857
 OY 716 QPNVQFC-IVALVI-I-FCSTITLCLVFEVKLITLRTNPDATONRR 759

RESULT 10
 ID R72092 standard; Protein: 912 AA.
 AC R72092; 1995 (first entry)
 DT 26-SEP-1995
 DE Human mglur4.
 KW Human metabotropic glutamate receptor subtype 4; mglur4; hmglur4;
 OS Homo sapiens.
 PN WO9508627-A.
 PD 30-MAR-1995.
 PF 07-SEP-1994; E02991.
 PR 20-SEP-1993; EP-810663.
 PR 19-AUG-1994; GB-016553.
 PA (CIBA) CIBA GEIGY AG.
 PI Flor PJ, Knoepfel T, Kuhn R, Lindauer K, Puettnner I;
 DR WPI; 95-139596/18.
 DR N-PSDB; 089342.
 PT Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and
 PT 7 - also corresp. DNA and antibodies, useful for identifying
 PT cpds. which modulate signal transduction activity
 PS Claim 2; Page 44-48; 110pp; English.
 CC Human metabotropic glutamate receptor subtype 4 (hmglur4) cDNA
 CC clones were isolated from a cerebellum cDNA library using a rat
 CC cDNA probe. Clone cmr20 lacked the 5' end of the hmglur4 gene.
 CC PCR using human genomic or brain cDNA as template was used to
 CC obtain a complete gene sequence (given in 089342) encoding hmglur4
 CC (R72092). Recombinant hmglur4 was produced in mammalian cells.
 SO Sequence 912 AA;

Query Match 3.3%; Score 228; DB 1; Length 912;
 Best Local Similarity 21.6%; Pred. No. 5.32e-07;
 Matches 62; Conservative 98; Mismatches 100; Indels 27; Gaps 22;

Db 588 AVLPFLAVVG-IAATLEVVITFVRKNDPTIVKASGRELSTVLLAGIFLCYATTEL--M- 643
 OY 483 SLISA-LTILGIMASAFLEFN-INKRNOKLIKSSPYMNNLITLIGMISYASIFLEGLD 540
 Db 644 ---IAEPDLGT-CSLRRIEFLGMSISYALLTKTNRIYRIFEOGRSAPFISPASQ 699
 OY 541 GSPFVSEKTEFTLCTVRWILLVGTTFAGFAKTMVHAIFKNVK--MKK-KIIOQKL 597
 Db 700 LAIFSLISLQI-LGICWFWVPSHSVVD-FODQRTLDPR-PA-RGVLK-CDMSDLSL- 753
 OY 598 LVIYVGMILLDLCILIC-WQAVDPLRTVEKYSMEPDPAIRODISIPLEHCENTHMTIIV 656
 Db 754 ICLL-GYSMLLMV-TC-TVYAIKTRGVPEFNEAKRPIGFMTYTTCIYWLAFIPIFGTSQ 810
 OY 657 LGIYVAAKGLIMLEFGCLAMETRNVSIP-ALNDSKYIGMSVYVNGIMCIIIGAAVSFLTRD 715
 Db 811 SADKLXIQTTLTIVSVLSASVSLGMLYMPKYYIILFHPQONVPRK 857

OY 716 QPNVQFC-IVALVI-I-FCSTITLCLVFEVKLITLRTNPDATONRR 759

RESULT 11
 ID R72095 standard; Protein: 481 AA.
 AC R72095;
 DT 26-SEP-1995 (first entry)
 DE Human mglur7 clone cmr5.
 KW Human metabotropic glutamate receptor subtype 4; mglur7; hmglur7;
 OS Homo sapiens.
 PN WO9508627-A.
 PD 30-MAR-1995.
 PF 07-SEP-1994; E02991.
 PR 20-SEP-1993; EP-810663.
 PR 19-AUG-1994; GB-016553.
 PA (CIBA) CIBA GEIGY AG.
 PI Flor PJ, Knoepfel T, Kuhn R, Lindauer K, Puettnner I;
 DR WPI; 95-139596/18.
 DR N-PSDB; 089345.
 PT Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and
 PT 7 - also corresp. DNA and antibodies, useful for identifying
 PT cpds. which modulate signal transduction activity
 PS Claim 8; Page 69-72; 110pp; English.
 CC Human metabotropic glutamate receptor subtype 7 (hmglur7) cDNA
 CC clones were isolated from cDNA libraries using a rat mglur4 probe.
 CC Fetal brain partial cDNA clone cmr5, encoding the protein given in
 CC R72095, was obtained. The missing 5' region of the clone was
 CC generated by PCR from brain cDNA. Sequence comparison of fetal
 CC brain and hippocampus clones indicated the existence of 2 subtypes
 CC of hmglur7 (R72097-98).
 SO Sequence 481 AA;

Query Match 3.1%; Score 214; DB 1; Length 481;
 Best Local Similarity 22.9%; Pred. No. 5.34e-06;
 Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;

Db 172 LAMLGIT-ATIFVMAFFIRYNDPTIVRASGRELSTVLLAGIFLCY-ITTF-I--MTA- 223
 OY 488 LTILGIMASAFLEFN-INKRNOKLIKSSPYMNNLITLIGMISYASIFLGDSFVSE 546
 Db 224 KPDVAVCSFRVFLGIMCISYALLTKTNRIYRIFEOGRSAPFISPASQ 283
 OY 547 KTFEFTLCTVRWILLVGTTFAGFAKTMVHAIFKNVK-K--KIIOQKLVIYCG 603
 Db 284 LISVOLLGFI-WFGVDPNNIID-YD-EHKTMNPGA-RGVLK-CDITDLOI-ICSL-G 336
 OY 604 MLTIDL-CILICQAVDPLRTVEKYSMEPDPAIRODISIPLEHCENTHMTIYIYA 662
 Db 337 YSILIMV-TC-TVYAIKTRGVPEFNEAKRPIGFMTYTTCIYWLAFIPIFGTAQSAEKLY 394
 OY 663 YKGLIMLEFGCLAMETRNVSIPA-LNDSKYIGMSVYVNGIMCIIIGAAVSFLTRDPNVQF 721
 Db 395 IOTTTLTISNLSASVALGMLYMPKYYIILFPELVQKRKRSF 438
 OY 722 C-IVALVI-I-FCSTITLCLVFEVKLITLRTNPDATONRRQF 762

RESULT 12
 ID R72093 standard; Protein: 867 AA.
 AC R72093;
 DT 26-SEP-1995 (first entry)
 DE Human mglur7 clone cmr2.
 KW Human metabotropic glutamate receptor subtype 4; mglur7; hmglur7;
 OS Homo sapiens.
 PN WO9508627-A.
 PD 30-MAR-1995.
 PF 07-SEP-1994; E02991.
 PR 20-SEP-1993; EP-810663.
 PR 19-AUG-1994; GB-016553.
 PA (CIBA) CIBA GEIGY AG.
 PI Flor PJ, Knoepfel T, Kuhn R, Lindauer K, Puettnner I;


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Db 597 IAMLGII-ATIFVMAFIRNDPIVRSAGRELSVLTGLPLCY--ITTF-L--MTA-648
Qy 488 LTIIGMIMASAFLEFN-IKRNRKLIKSSPNNNLIIGMLSTASIFLGLDGSFVSE 546
Db 649 KPDVAVCSFRFVFLGIMCISYVALLTKNRIYRIFEOGKSVTPRLISPTSLATSS 708
Qy 547 KTFETLCTVFWILTWGYTAFGAFKAKTWVHAIFKNVKKM-K--KLIKDKLLVIYGG 603
Db 709 LISVOLLGVFI-WGVDPPIIID-YD-EHKTMNPEQA-RGVLK-CDITDLOI-ICSL-G 761
Qy 604 MLTIDL-CLICQWADVPLRRTVEKTSMEPDAGRDISIRPLEHCENTHMTWLGIVYA 662
Db 762 YSILLAV-TC-TYVAIKTRGVNPNENAKPIGFTWYTCIWLAFIPIFGTAQSAEKLY 819
Qy 663 YKGLIMFGCFLEMETRNVSIPA-LNDSKYICMSYVNGVICIGAAVSFLTRDQPNVOF 721
Db 820 IQTTTLTISNLSASVALGMLYMPKYYIIIFHELNVOKKRRSF 863
Qy 722 C-YVALVI-I-FCSTITLCLVFPVKLITLTNPDAATQNRROF 762

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RESULT 15

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ID R72098 standard; Protein; 922 AA.
AC R72098;
DE 26-SEP-1995 (first entry)
DE Human mglur7b.
KW Human metabotropic glutamate receptor subtype 4; mglur7; hmglur7;
KW signal transducer.
OS Homo sapiens.
PN WC9508627-A.
PD 30-MAR-1995.
PE 07-SEP-1994; E02991.
PR 20-SEP-1993; EF-810663.
PR 19-AUG-1994; GB-016533.
PA (CIBA ) CIBA GEIGY AG.
PI Flor PJ, Knoepfel T, Kuhn R, Lindauer K, Puetner I;
DR WPI; 95-139596/18.
DR N-PSDB; 089348.
PT Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and
PT 7 - also corresp. DNA and antibodies, useful for identifying
PT cpds. which modulate signal transduction activity
PS Claim 7; Page 95-99; 110pp; English.
CC Human metabotropic glutamate receptor subtype 7 (hmglur7) cDNA
CC clones were isolated from fetal brain and hippocampus cDNA libraries
CC using a rat mglur4 probe, and the 5' region missing from these
CC clones was generated by PCR from brain cDNA. Sequence comparison of
CC fetal brain and hippocampus clones indicated the existence of 2
CC subtypes of hmglur7, hmglur7a (given in R72097) and hmglur7b
CC (R72098). Full-length cDNA clones (Q89347-48) encoding these
CC proteins were expressed in mammalian cells.
SQ Sequence 922 AA;

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Query Match 3.1%; Score 214; DB 1; Length 922;

Best Local Similarity 22.9%; Pred. No. 5,34e-06;

Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;

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Db 597 IAMLGII-ATIFVMAFIRNDPIVRSAGRELSVLTGLPLCY--ITTF-L--MTA-648
Qy 488 LTIIGMIMASAFLEFN-IKRNRKLIKSSPNNNLIIGMLSTASIFLGLDGSFVSE 546
Db 649 KPDVAVCSFRFVFLGIMCISYVALLTKNRIYRIFEOGKSVTPRLISPTSLATSS 708
Qy 547 KTFETLCTVFWILTWGYTAFGAFKAKTWVHAIFKNVKKM-K--KLIKDKLLVIYGG 603
Db 709 LISVOLLGVFI-WGVDPPIIID-YD-EHKTMNPEQA-RGVLK-CDITDLOI-ICSL-G 761
Qy 604 MLTIDL-CLICQWADVPLRRTVEKTSMEPDAGRDISIRPLEHCENTHMTWLGIVYA 662
Db 762 YSILLAV-TC-TYVAIKTRGVNPNENAKPIGFTWYTCIWLAFIPIFGTAQSAEKLY 819
Qy 663 YKGLIMFGCFLEMETRNVSIPA-LNDSKYICMSYVNGVICIGAAVSFLTRDQPNVOF 721
Db 820 IQTTTLTISNLSASVALGMLYMPKYYIIIFHELNVOKKRRSF 863

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Qy 722 C-YVALVI-I-FCSTITLCLVFPVKLITLTNPDAATQNRROF 762

Search completed: Wed Apr 19 21:49:31 2000
Job time : 261 secs.